

GenCore version 5.1.1.6  
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OR N 2 - Nucleic search, using sw model  
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(without alignments)  
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Listing first 45 summaries

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- 1: gb.ba.\*
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ad. do. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3580.2	56.2	5653	6	I95540	I95540 Sequence 1 from patent US 5733543
2	3580.2	56.2	5900	6	AX573107	AX573107 Sequence 1 from patent US 5733543
3	3578.4	56.1	5432	6	BD234590	BD234590 Sequence 1 from patent US 5733543
4	3578.4	56.1	5432	6	AX026821	AX026821 Sequence 1 from patent US 5733543
5	3578.4	56.1	5446	6	AX319694	AX319694 Sequence 1 from patent US 5733543
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7	3578.4	56.1	5639	12	AX437643	AX437643 Sequence 1 from patent US 5733543
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9	3578.4	56.1	6180	6	AX207724	AX207724 Sequence 1 from patent US 5733543
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12	3578.4	56.1	6277	12	AX437644	AX437644 Sequence 1 from patent US 5733543
13	3578.4	56.1	6331	12	EVPICMVP1	EVPICMVP1 Sequence 1 from patent US 5733543
14	3578.4	56.1	6333	12	EVPICMVP3	EVPICMVP3 Sequence 1 from patent US 5733543
15	3578.4	56.1	6335	12	EVPICMVP2	EVPICMVP2 Sequence 1 from patent US 5733543
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22	3578.4	56.1	6436	6	AX207740	AX207740 Sequence 1 from patent US 5733543
23	3578.4	56.1	6459	6	AX207749	AX207749 Sequence 1 from patent US 5733543
24	3578.4	56.1	6459	6	AX207755	AX207755 Sequence 1 from patent US 5733543
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ALIGNMENTS

RESULT 1

LOCUS	I95540	5653 bp	DNA	linear	PAT	US 5733543
DEFINITION	Sequence 1 from patent US 5733543.					
ACCESSION	I95540					
VERSION	I95540.1	GI:3940010				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 5653)					
AUTHORS	Nabel,G.J., Woffendin,C., Yang,N.-S. and Sheehy,M.J.					
TITLE	Introduction of HIV-protective genes into cells by particle-mediated gene transfer					
JOURNAL	Patent: US 5733543-A 1 31-MAR-1998;					

## Location/Qualifiers

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Conservative 0; Mismatches 63; Indels 470; Gaps 7;  
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3107.1 GI:26005046

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erford, C., Gray, J.T., Lee, J.S. and Mulligan, R.C.  
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Children's Medical Center Corporation (US) ; PRESIDENT AND  
OWS OF HARVARD COLLEGE (US)

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AUTHORS 1 (bases 1 to 5432)  
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Best Local Similarity 88.9%; Pred. No. 0;  
Matches 4141; Conservative 0; Mismatches 16; Indels 503;  
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SO:R					
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AC:UT					
CO:					
FE:IT					
OR:G					
AC:le					
la					
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QY 4896 CGACCGCTGCGCTTATCGGTAATCATGCTTGTGAGTCCAAACCGGTAAGACA  
Db 3967 CGACCGCTGCGCTTATCGGTAATCATGCTTGTGAGTCCAAACCGGTAAGACA



QY	1958	A	CGCCACTGGCAGCAGCCACTGGTTAA	CAGGATTACGACAGCGAGGTATGTTAGCGGTGC	5015
DB	1027	A	CGCCACTGGCAGCAGCCACTGGTAA	CAGGATTACGACAGCGAGGTATGTTAGCGGTGC	4086
QY	4016	T	CAGAGTTCTTGAAGTGGTGGCCTAACTAC	CGCTACACTAGNAGAACAGTATTTGGTAT	5075
DB	1087	T	CAGAGTTCTTGAAGTGGTGGCCTAACTAC	CGCTACACTAGNAGAACAGTATTTGGTAT	4146
QY	1079	C	CGCGCTCTGCTGAAGCAGGTACCTTCG	GAAGAGTGTGGTAGCTCTTTGATCCGGCAA	5135
DB	1147	C	CGCGCTCTGCTGAAGCAGGTACCTTCG	GAAGAGTGTGGTAGCTCTTTGATCCGGCAA	4206
QY	1336	A	AAACCAACCGCTGGTAGCGGTGGTTTTT	TGTTGCAAGCAGCAGATTACGCGCAGAAA	5195
DB	1207	A	AAACCAACCGCTGGTAGCGGTGGTTTTT	TGTTGCAAGCAGCAGATTACGCGCAGAAA	4266
QY	1916	A	AAGGATCTCAAGAGATCCCTTTGATCTT	TCATCGGGTCTGACGCTCAGTGGAACGA	5255
DB	1267	A	AAGGATCTCAAGAGATCCCTTTGATCTT	TCATCGGGTCTGACGCTCAGTGGAACGA	4326
QY	1258	A	ACTCACGTTAAGGGATTTTGGTCA	TGAGATTCAAAAAGGATCTTCACTAGATCCT	5315
DB	1327	A	ACTCACGTTAAGGGATTTTGGTCA	TGAGATTCAAAAAGGATCTTCACTAGATCCT	4386
QY	5318	T	TAAATTAAATGAAGTTTAAATCAATCTA	AAAGTATATATAGTAAACTTTGGTCTGA	5375
DB	1387	T	TAAATTAAATGAAGTTTAAATCAATCTA	AAAGTATATATAGTAAACTTTGGTCTGA	4446
QY	3374	C	GTTACCAATGCTTAATCAGTCAGGCAC	CTATCTCAGCGATCTGTCTATTTTCGTTCA	5435
DB	1447	C	GTTACCAATGCTTAATCAGTCAGGCAC	CTATCTCAGCGATCTGTCTATTTTCGTTCA	4506
QY	5438	C	ATAGTTGCTGACTCCCGTCTGTAGATA	AACTACGATACGGAGGGCTTACCATCTGG	5495
DB	1507	C	ATAGTTGCTGACTCCCGTCTGTAGATA	AACTACGATACGGAGGGCTTACCATCTGG	4566
QY	5498	C	CCAGTGTCTGCAATGATACCGCGAGAC	CCACGCTCACCGGCTCCAGATTATCAGCAAT	5555
DB	1567	C	CCAGTGTCTGCAATGATACCGCGAGAC	CCACGCTCACCGGCTCCAGATTATCAGCAAT	4626
QY	5557	A	ACCAGCCAGCCGAGCGCCGAGCGCAGA	AGTGGTCTTGCAACTTTATCCCGCTCCAT	5615
DB	1627	A	ACCAGCCAGCCGAGCGCCGAGCGCAGA	AGTGGTCTTGCAACTTTATCCCGCTCCAT	4686
QY	5614	C	AGTCTATTAAATTTGTTCCGGGAAGCT	AGTAGTAAGTAGTTGCGCAGTTAATAGTTGCG	5675
DB	1687	C	AGTCTATTAAATTTGTTCCGGGAAGCT	AGTAGTAAGTAGTTGCGCAGTTAATAGTTGCG	4746
QY	5674	C	AGTGTGTTCGCAATGCTACGGCATCGT	GGTGTCACGCTCGTTCGTTTCGGTAGCGCTC	5735
DB	1747	C	AGTGTGTTCGCAATGCTACGGCATCGT	GGTGTCACGCTCGTTCGTTTCGGTAGCGCTC	4806
QY	5737	A	TCAGCTCCGGTTTCCAAACGATCAAG	CGCAGTTACATGATCCCGCATGTTTGCAGAAA	5795
DB	1807	A	TCAGCTCCGGTTTCCAAACGATCAAG	CGCAGTTACATGATCCCGCATGTTTGCAGAAA	4866
QY	5737	A	GGGGTTAGCTCTCTTCGGTCTCCGAT	TCGTTGTCAAGTAAGTGTGGCGCGAGTGTATC	5855
DB	1867	A	GGGGTTAGCTCTCTTCGGTCTCCGAT	TCGTTGTCAAGTAAGTGTGGCGCGAGTGTATC	4926
QY	5857	A	CTCATCGTTATGCGACCATGCGATAAT	CTCTTACTGTATGCGCATCCGTAGATGCTTT	5915
DB	1927	A	CTCATCGTTATGCGACCATGCGATAAT	CTCTTACTGTATGCGCATCCGTAGATGCTTT	4986
QY	5917	T	CTGTGACTGGTAGTACTCAACCAAGT	CAATCTCTGAGAAATGTTATGCGGCGACCGAG	5975
DB	1987	T	CTGTGACTGGTAGTACTCAACCAAGT	CAATCTCTGAGAAATGTTATGCGGCGACCGAG	5046
QY	5977	T	TGCTTTGCCCGGGTCTCAATACGGGATA	ATACCGCGCCACATAGCAGAACTTTTAAAGT	6035
DB	2047	T	TGCTTTGCCCGGGTCTCAATACGGGATA	ATACCGCGCCACATAGCAGAACTTTTAAAGT	5106

Qy	6036	GCTCATCATTTGGAAACAGTTCTTCGGGGCGAAACACTCTCAAGGATCTTACCGCT	6098
Db	5107	GCTCATCATTTGGAAACAGTTCTTCGGGGCGAAACACTCTCAAGGATCTTACCGCT	5166
Qy	6096	ATCCAGTTTCGATGTAACCCCACTCGTGCACCACTGATCTTTCAGCATCTTTTAC	6155
Db	5167	ATCCAGTTTCGATGTAACCCCACTCGTGCACCACTGATCTTTCAGCATCTTTTAC	5226
Qy	6156	CAGCGTTTCTGGGTGAGCAAAAAACAGGAAGCGCAAAATGCCGCAAAAAGGGAAT	6276
Db	5227	CAGCGTTTCTGGGTGAGCAAAAAACAGGAAGCGCAAAATGCCGCAAAAAGGGAAT	5286
Qy	6216	GACACGGAATGTTGAATACATCATCTCTTCTTCTTTCATATATTTGAAGCAT	6276
Db	5287	GACACGGAATGTTGAATACATCATCTCTTCTTCTTTCATATATTTGAAGCAT	5346
Qy	6276	GGGTATTGTCTCATGAGCGGATACATATTTGAATGTTATTAGAAAAATAAACA	6335
Db	5347	GGGTATTGTCTCATGAGCGGATACATATTTGAATGTTATTAGAAAAATAAACA	5406
Qy	6336	GGTTCGCGCACATTTCCCGGAAAAGTGCCACCTGACGTC	6375
Db	5407	GGTTCGCGCACATTTCCCGGAAAAGTGCCACCTGACGTC	5446
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|||||TTGCCAGCGCCCTAGCGCCGCTCTTTTGGCTTCTTCCCTTCTCGCCAGCTT 1435  
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|TAGGCACCTCGACCCCAAAAACCTTGAATTAGGGTGATGGTTCCAGCTAGTGGGCCATC 2048  
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|CTGATAGACGGTTTTTTCGCGCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACT 2108  
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|CCAGGCAGGCAGAGTATCAAAAGCATGTCATCTCAATTAGTCAGCAACCCAGGTGTGA 1847  
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|GTCCCGAGGCTCCCGCAGGAGAGTATGCAAGCATGTCATCTCAATTAGTCAGCA 1907  
|CATAGTCCCGCCCTAACTCCGCCCATCCCGCCCTTAATCTCCGCCAGTTCGCCCCAT 2527  
|CATAGTCCCGCCCTAACTCCGCCCATCCCGCCCTTAATCTCCGCCAGTTCGCCCCAT 1967  
|TCGGCCCATAGTGTGCTAAATTTTATTTATGTCAGAGGCCGAGGCCCTCGGCC 2587  
|TCGGCCCATAGTGTGCTAAATTTTATTTATGTCAGAGGCCGAGGCCCTCGGCC 2027  
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|TGAGCTATTCCAGAGTAGTAGGAGGCTTTTTCGAGGCCCTAGGCTTTTGCAAGAT 2087  
|-----GATCAAGAGACAGGATGAGGATCGTTT 2675  
|CCCGGAGCTTGATATCCATTTTCGGATCTGATCAAGACAGGATGAGGATCGTTT 2147  
|CATGATTGAACGAAGTGAATGCAACGAGGTTCTCCGCCCTTCGGGTGGAGAGGCTA 2735  
|CATGATTGAACGAAGTGAATGCAACGAGGTTCTCCGCCCTTCGGGTGGAGAGGCTA 2207  
|GGCTATGACTGGGCACACAGCAATCGGCTGCTCTGATGCGCGGCTTTCCGGCTG 2795  
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Db 2388 GTGCTCGACGCTGTCTACCTGAAGCGGAAGGACTGGCTGCTATTTTGGGCGAAGTC  
QY 2976 CAGGATCTCTGTGTCACTCTCACCTTGTCTCTCGCGAGAAAGTATCCATCATGGCT  
Db 2448 CAGGATCTCTGTGTCACTCTCACCTTGTCTCTCGCGAGAAAGTATCCATCATGGCT  
QY 3036 ATGCGGGGCTGCATAGCTTGTATCGGCTTACCTGCCCATTTCGACCAACGAGCG  
Db 2508 ATGCGGGGCTGCATAGCTTGTATCGGCTTACCTGCCCATTTCGACCAACGAGCG  
QY 3096 CGCATTCGAGCGAGCAGCAGCTACTTCGATGGAAGCCGCTCTTGTGATCAGGATGAT  
Db 2568 CGCATTCGAGCGAGCAGCAGCTACTTCGATGGAAGCCGCTCTTGTGATCAGGATGAT  
QY 3156 GAAAGCATCAGGGGCTTCGCGCAGCGGAACTGTTTCGCGAGGCTCAAGCGGAGCG  
Db 2628 GAAAGCATCAGGGGCTTCGCGCAGCGGAACTGTTTCGCGAGGCTCAAGCGGAGCG  
QY 3216 GACCGCGAGGATCTCGTCTGTCGACCATGCGGATGCTTGTTCGCGAATATCATG  
Db 2688 GACCGCGAGGATCTCGTCTGTCGACCATGCGGATGCTTGTTCGCGAATATCATG  
QY 3276 AATGCGCGCTTTCTGGAATCATCGACTGTGCGCGGCTGGGTGTGGGAGCCGC  
Db 2748 AATGCGCGCTTTCTGGAATCATCGACTGTGCGCGGCTGGGTGTGGGAGCCGC  
QY 3336 GACATAGGTTGGCTACCCGTGATATTGCTGAGAGGCTTGGCGGCGAATGGGCT  
Db 2808 GACATAGGTTGGCTACCCGTGATATTGCTGAGAGGCTTGGCGGCGAATGGGCT  
QY 3396 TTCTCTGTGCTTTTACGGTATCGCGCTCCCGATTCGCGAGCGCATCGGCTTCTAT  
Db 2868 TTCTCTGTGCTTTTACGGTATCGCGCTCCCGATTCGCGAGCGCATCGGCTTCTAT  
QY 3456 CTTGACAGGTTCTTCTGAGCGGAGCTCTGGGTTTGAATAAGCGAACAGCGA  
Db 2928 CTTGACAGGTTCTTCTGAGCGGAGCTCTGGGTTTGAATAAGCGAACAGCGA  
QY 3516 ACCTGCGCATCAAGATTTTCGATTCACCGCGCTTCTATGAAGGTTGGGCT  
Db 2988 ACCTGCGCATC-----  
QY 3576 TCGTTTTTCGCGAGCGCGGCTGGATGATCCTCCAGCGCGGGATCTCATGCTGG  
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QY 3636 TCGCCCAACCTTAGGGGAGGCTAACTGAACAACGGAAGAGACAAATACCGGAAG  
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QY 3696 GCGCATGACGGCAATAAAGACAGATAAAGCGACGGTGTGGGTCTGTTGT  
Db 2998 -----  
QY 3756 ACGCGGGGTTCCGCTCCAGGGCTGGCACTCTGTGATACCCACCGAGACCCCA  
Db 2998 -----  
QY 3816 CCAATAGCGCGGTTTCTTCTTTTCCCCCACCCCAAGTTTCGGGTGA  
Db 2998 -----  
QY 3876 AGGGCTCGCAGCCAACTCGGGGCGGAGGCCCTGCCATAGCTCAGTGTCTAG  
Db 2998 -----ACG#  
QY 3936 CGATTCCAACGCGCGCTTCTATGAAGGTTGGGCTTCGGAATCGTTTTCGGGA  
Db 3007 CGATTCCAACGCGCGCTTCTATGAAGGTTGGGCTTCGGAATCGTTTTCGGGA  
QY 3996 CTGATGATCTCCAGCGGGGATCTCATGCTGGAGTCTTTCGCCCAACCCCA  
Db 3067 CTGATGATCTCCAGCGGGGATCTCATGCTGGAGTCTTTCGCCCAACCCCA

[illegible]

Qy	5136	ACAAACACACCGCTGGTAGCGGTGGTTTTTTTGGTTGGACGACAGATTACCGG	5137
Db	4207	ACAAACACACCGCTGGTAGCGGTGGTTTTTTTGGTTGGACGACAGATTACCGG	4208
Qy	5196	AAAAGGATCTCAAGAGATCCTTTTGATCTTTTCTACGGGCTCTGAGCCTCAGTG	5200
Db	4267	AAAAGGATCTCAAGAGATCCTTTTGATCTTTTCTACGGGCTCTGAGCCTCAGTG	4271
Qy	5256	AAACTCTACGTTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACTTA	5260
Db	4327	AAACTCAGCTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACTTA	4338
Qy	5316	TTTAAATTAATAATGAAGTTTTAAATCAATCTAAAGTATATATAGTAAACTTGG	5320
Db	4387	TTTAAATTAATAATGAAGTTTTAAATCAATCTAAAGTATATATAGTAAACTTGG	4398
Qy	5376	CAGTTACCAATGCTTAATCAGTCAGGCACCTATCTCAGCGCATCTGTCTATTTCC	5380
Db	4447	CAGTTACCAATGCTTAATCAGTCAGGCACCTATCTCAGCGCATCTGTCTATTTCC	4458
Qy	5436	CATAGTTGCGTGAATCCCGCTCGTGTAGATAAATCTACGATACGGAGGGCTTACC	5440
Db	4507	CATAGTTGCGTGAATCCCGCTCGTGTAGATAAATCTACGATACGGAGGGCTTACC	4518
Qy	5496	CCCAGTGTGCAATGATACGGGAGACCCACGCTACACGGCTCCAGATTATCT	5499
Db	4567	CCCAGTGTGCAATGATACGGGAGACCCACGCTACACGGCTCCAGATTATCT	4578
Qy	5556	AAACCCAGCCGGAAGGGCCGAGCGCAGAAGTGTCCTGCACACTTATTCGCC	5560
Db	4627	AAACCCAGCCGGAAGGGCCGAGCGCAGAAGTGTCCTGCACACTTATTCGCC	4638
Qy	5616	CCAGTCTATTAAATTTGTTCCGGGAAGCTAGAGTAAGTAGTTTCGCCAGTTAATAG	5620
Db	4687	CCAGTCTATTAAATTTGTTCCGGGAAGCTAGAGTAAGTAGTTTCGCCAGTTAATAG	4698
Qy	5676	CAACGTTGTTGGCAATTCGTCAGGCATCGTGGTGTCACGCTCGTCGTTTGGTAT	5680
Db	4747	CAACGTTGTTGGCAATTCGTCAGGCATCGTGGTGTCACGCTCGTCGTTTGGTAT	4758
Qy	5736	ATTCAGCTCCGGTTCCCAACGATCAAGCGCAGTTACATGATCCCCCATGTTGTG	5740
Db	4807	ATTCAGCTCCGGTTCCCAACGATCAAGCGCAGTTACATGATCCCCCATGTTGTG	4818
Qy	5796	AGCGGTTAGCTCCCTTCGGTCTCCCGATCGTTGTCTCAGAAGTAAGTTGGCCGAGT	5800
Db	4867	AGCGGTTAGCTCCCTTCGGTCTCCCGATCGTTGTCTCAGAAGTAAGTTGGCCGAGT	4886
Qy	5856	ACTCATGGTTATGGCAGACATGCAATAATCTCTTACTGTCAATGCCATCCGTAAG	5860
Db	4927	ACTCATGGTTATGGCAGACATGCAATAATCTCTTACTGTCAATGCCATCCGTAAG	4943
Qy	5916	TTCTGTGACTGGTCAGTACTCAACCAAGTCAATCTGAGATAGTGTATCGGGCG	5920
Db	4987	TTCTGTGACTGGTCAGTACTCAACCAAGTCAATCTGAGATAGTGTATCGGGCG	5000
Qy	5976	TTGCTCTTGGCCGGCGTCAATACGGGATATAACCGCGCCATACAGCAGAACTTT	5980
Db	5047	TTGCTCTTGGCCGGCGTCAATACGGGATATAACCGCGCCATACAGCAGAACTTT	5068
Qy	6036	GCTCATCATTTGGAAAAAGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCT	6040
Db	5107	GCTCATCATTTGGAAAAAGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCT	5128
Qy	6096	ATCCAGTTCGATGTAAACCACTCGTGACCCCACTGATCTTTCAGCATCTTTTAC	6100
Db	5167	ATCCAGTTCGATGTAAACCACTCGTGACCCCACTGATCTTTCAGCATCTTTTAC	5188
Qy	6156	CAGCGTTTCTGGGTGACAAAAACAGGAAGGCAAAATCCGCCAAAAAGGGAAT	6160
Db	5227	CAGCGTTTCTGGGTGACAAAAACAGGAAGGCAAAATCCGCCAAAAAGGGAAT	5256
Qy	6216	GACACGGAAATGTTGAATACTCATACTCTTCCTTTTTTCAATATTATTGAAGCAT	6220

Conservative	56.1%; 88.9%; 0;	Score 3578.4;	DB 12;	Length 5639;	16;	Indels 503;	Gaps 5;
ICTCCACGCTTTTCTGAGCGGAAAGAACACAGCTGGGGGTCTAGGGGGTATCCCCACGC							1809
ICTCTATGGCTTCTGAGCGGAAAGAACACAGCTGGGGTCTAGGGGGTATCCCCACGC							1508
ICTGTATAGCGCGCATTAAGCGCGCGGGTGTGGTGTACGCGCAGCGTGAACGCTTAC							1869
ICTGTATAGCGCGCATTAAGCGCGCGGGTGTGGTGTGTACGCGCAGCGTGAACGCTTAC							1568
TTGCCACGCGCCTTAGCGCCCGCTCCTTTTGGCTTTCTCCCTTCTCTTCTCGCCACGTT							1929
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TGGGCTTTCGGCGTCAAGCTCTAAATCGGGC-TCCCTTTAGGGTTCGATTAGTATGTC							1988
CGGGCTTTCGGCGTCAAGCTCTAAATCGGGCATCCCTTTAGGGTTCGATTTAGTATGTC							1688

Db 1701 ATGCGGCGCTGCATACGCTTGTATCGGCTACTCGCCATTCGACCAACGAAACAT 2760  
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 Db 1761 CGCATCGAGCGAGCAGTACTCGGATGGAAGCGGCTTGTGTCAGTACAGATCATCTGGAC 2820  
 QY 1156 GAAGAGCATCAGGGGCTCGCGCAGCGCAACTGTGTGCGCAGGCTCAAGCGGAGCATGCC 3215  
 Db 1821 GAAGAGCATCAGGGGCTCGCGCAGCGCAACTGTGTGCGCAGGCTCAAGCGGAGCATGCC 2880  
 QY 1216 GACGCGGAGGATCTCGTGTGTGACCATGCGGATGCGCTGCTCCGGAATATCATGTGGAA 3275  
 Db 1881 GACGCGGAGGATCTCGTGTGTGACCATGCGGATGCGCTGCTCCGGAATATCATGTGGAA 2940  
 QY 1276 AATGCGCGCTTTCTTGGAATTCATCGACTGTGCGCGGCTGGGTGTGCGGACCGCTATCAG 3335  
 Db 1941 AATGCGCGCTTTCTTGGAATTCATCGACTGTGCGCGGCTGGGTGTGCGGACCGCTATCAG 3000  
 QY 1336 GACATAGCGTTGGCTACCGGTGATATTCCTGAAGAGCTTGGCGGGAATGGGCTGACCGC 3395  
 Db 1001 GACATAGCGTTGGCTACCGGTGATATTCCTGAAGAGCTTGGCGGGAATGGGCTGACCGC 3060  
 QY 1396 TTCTCTGCTGCTTACGATCGCGCTCCGATTCGCGAGCGCATCGCCTTCTATCGCCTT 3455  
 Db 1061 TTCTCTGCTGCTTACGATTCGCGCTCCGATTCGCGAGCGCATCGCCTTCTATCGCCTT 3120  
 QY 1456 CTGTGACGAGTCTTCTGAGCGGAGCTCTCGGGTTCGAAATGACCGACCAAGCGAGCGCCA 3515  
 Db 1121 CTGTGACGAGTCTTCTGAGCGGAGCTCTCGGGTTCGAAATGACCGACCAAGCGAGCGCCA 3180  
 QY 1516 ACCTGCCATCAGCAGATTTTCGATTCACCGCGCCTTCTATGAAGGTTGGGCTTCGGAA 3575  
 Db 1181 ACCTGCCATC----- 3190  
 QY 1576 TCGTTTTCGGGACCGCGGCTGGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTTCT 3635  
 Db 1191----- 3190  
 QY 1636 TCGCCCACTAGGGGAGGCTAACTGAACACAGGAAGGAGCAATACCGGAAGGAACCC 3695  
 Db 1191----- 3190  
 QY 1696 GCGCATGACGGCAATAAAAGACAGAAATAAAGCGATGTTGGGTGCTTGTTCATAA 3755  
 Db 1191----- 3190  
 QY 1756 ACGCGGGTTCCGTCCAGGGCTGGCACTCTGTCTGATACCCACCGAGACCCCATTTGGGG 3815  
 Db 1191----- 3190  
 QY 1816 CCAATACGCGCGGTTTCTTCTTTTCCACCCACCCCAAGTTCCGGTGAAGGCC 3875  
 Db 1191----- 3190  
 QY 1876 ACGGCTCGAGCCAAAGTCGGGCGGAGCGCCCTGCAATAGCTCAGTGTACGAGATTT 3935  
 Db 1191-----ACGAGATTT 3199  
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 AUTHORS Vekris,A., Masse,K. and Arveiler,B.  
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 JOURNAL Submitted (24-FEB-1997) Lab. Pathologie Molculaire et T  
 Genique, Universite de Bordeaux II, 146, rue Leo Saignat  
 33076, France  
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RESULT 11			
LOCUS	BD168966	6238 bp	DNA linear PAT 10 MAR 2003
DEFINITION	Method of searching for gene encoding nuclear transport		
ACCESSION	BD168966		
VERSION	BD168966.1	GI:27874778	
KEYWORDS	WO 0236823-A/1.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 6238)		
AUTHORS	Maekawa,T., Mori,M. and Takahara,Y.		
TITLE	Method of searching for gene encoding nuclear transport		
JOURNAL	Patent: WO 0236823-A 1 10-MAY-2002;		
COMMENT	AJINOMOTO CO INC,TAKAMI MAEKAWA,MAIKO MORI,YOSHIYUKI TAKAHARA OS Artificial Sequence PN WO 0236823-A/1 PD 10-MAY-2002 PF 06-NOV-2001 WO 2001P009700 PRI 06-NOV-2000 JP 00P 337906 PI TAKAMI MAEKAWA,MAIKO MORI,YOSHIYUKI TAKAHARA PC C12Q1/68,G01N33/15,G01N33/50,C12N15/10 CC Description of Artificial Sequence: recombinant plasmid ES Key source Location/Qualifiers FT source 1..6238 FT /organism='Artificial Sequence', Location/Qualifiers 1..6238 /organism='synthetic construct' /mol_type='genomic DNA' /db_xref='taxon:32630'		
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source			
ORIGIN			
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Qy	1810	GCCCTGTAGCGGCGCATTAAGCGCGCGGGGTGTGGTGTACGCGCAGCGTGAC	1948

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QY 5676 CAGGTTGTTGCCATTGCTACAGGCATCGTGGTGTACCGCTCGCTGTGGTAA 5735  
DB |||||  
QY 5539 CAGGTTGTTGCCATTGCTACAGGCATCGTGGTGTACCGCTCGCTGTGGTAA 5598  
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DB |||||  
QY 5599 ATTCACTCCGTTCCCAACGATCAAGGGGAGTTACATGATCCCCCATGTTGT 5558  
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QY 5796 AGCGGTTAGTCTCCTCGGCTCTCCGATCGTTGTACAGTAAGTTGGCGCGAGT 5855  
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QY 5916 TTCTGTGACTGGTAGTACTCAACCAAGTCATTCTGAGAAATAGTGTATGCGGC 5975  
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DB |||||  
QY 5976 TTGCTCTTGGCGGCGTCAATACGGGATTAATACCGGCCACATAGCAGAACTTT 6045  
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QY 5839 TTGCTCTTGGCGGCGTCAATACGGGATTAATACCGGCCACATAGCAGAACTTT 5898  
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QY 5899 GCTCATCTTGGAAACAGTTCTTTCGGGCGGAAACTCTCAAGGATCTTACCGCT 5958  
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QY 5959 ATCCAGTTCGATTAACCCCACTCGTGACCCCAACTGATCTTACGATCTTTTAC 6019  
DB |||||  
QY 6156 CAGCGTTTCTTGGGTGAGCAAAAACAGGAAGGCAAAATGCGCGCAAAAAGGGAAT 6219  
DB |||||



Conservative	0; Mismatches	16; Indels	503; Gaps	5;
--------------	---------------	------------	-----------	----



309 TACGCGCAGGGCGCGCGTCTCTTTTGTCAAGACCGACCTGTCGGTGCCTGAAATGAA 3158  
3854 CTGCAAGACGAGGCGCGCTATCGTGGCTGGCCACGACGGCGCTTCTTTCGCGAGCT 2915  
315 CCGAGACGAGGCGCGCGCTATCGTGGCTGGCCACGACGGCGCTTCTTTCGCGAGCT 3218  
291 GCTCGAGCTTGTCTA CTGAGCGGGAAGGGA CTGGCTGCTATTGTTGGCGGAAGTTCGCGGG 2975  
321 GCTCGAGCTTGTCTA CTGAGCGGGAAGGGA CTGGCTGCTATTGTTGGCGGAAGTTCGCGGG 3278  
297 CAGGATCTCTGTCTATCTACCTTCTCTGCTGGCGGAGAAATATCCATCATGGCTATGCA 3035  
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303 ATGCGCGGCTGATACGCTTGTATCGGCTTACCTGCGCCATTCGACCAACCAAGGAAACAT 3095  
333 ATGCGCGGCTGATACGCTTGTATCGGCTTACCTGCGCCATTCGACCAACCAAGGAAACAT 3398  
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315 GAGAGCATCAGGGCTCGCGCCAGCGCAACTGTTGCGCAGGCTCAAGCGCGCATGCCCC 3215  
345 GAGAGCATCAGGGCTCGCGCCAGCGCAACTGTTGCGCAGGCTCAAGCGCGCATGCCCC 3518  
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351 GACGCGGAGGATCTCGTCTGTGACCCATGCGCATGCGCTTTCGCGCAATATCATGTGGAA 3578  
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357 AATGGCGGCTTTCTGGAATTCATCGACTGTGGCGCGCTGGTGTGGCGGACCCGCTATCAG 3638  
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381 ACTGCGCATC----- 3828  
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369 GCGCATCGCGCAATAAAGACAGAAATAAAACGACGGTGTGGGTGCTGTTGTTGTTATAA 3755  
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375 AXGCGGGGTTTCGGTCCCGAGGCTGGCACTCTGTGATACCCACCGAGACCCCATTTGGGG 3815  
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387 AXGGCTCGCAGCCAACTCGGGGGCGGCGCCCTGCCATAGCTCAGTGTCTACGAGATTT 3935

3829 -----ACCGAGCTT 3837  
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4296 AGCTCGGGTGGCTTAATGAGTGAGCTAATCTCACTTAATTTGGCTTTCGCTCCT 4355  
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4258 TTTCAGCTCGGGAACCTGTCTGCGAGCTGATTAATGAATCGGCAACGCGC 4317  
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4438 ATCAGGGGATACGCGAGGAAGAACTGTGAGCAAAAGGCGGAGCAAAAGGCCAC 4497  
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4656 AAATCGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATATCC 4715  
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4956 ATCGCCACTGGCAGAGCCACTCGTAAACAGGATTTAGCAGAGGAGGTATGTAGC 5015  
4858 ATCGCCACTGGCAGAGCCACTCGTAAACAGGATTTAGCAGAGGAGGTATGTAGC 4917

Qy	6096	ATCCAGTTTCGATGTAAACCCACTCGTGCCACCCAACTGATCTTTCAGCATCTTTTAA
Db	5998	ATCCAGTTTCGATGTAAACCCACTCGTGCCACCCAACTGATCTTTCAGCATCTTTTAA
Qy	6156	CACGGTTTCTGGGTGAGCAAAAAACAGAAAGGCCAAAATGCCGAAAAAAGGGAAAT
Db	6058	CACGGTTTCTGGGTGAGCAAAAAACAGAAAGGCCAAAATGCCGAAAAAAGGGAAAT
Qy	6216	GACACGGAAATGTTGAAATACTCATACTCTTCTCTTTTCAATATATTATGGAAGCAAT
Db	6118	GACACGGAAATGTTGAAATACTCATACTCTTCTCTTTTCAATATATTATGGAAGCAAT
Qy	6276	GGGTATATTGCTCATCAGCGGGATACATATTTGAAATGTTATTGAAAAAATAAACA
Db	6178	GGGTATATTGCTCATCAGCGGGATACATATTTGAAATGTTATTGAAAAAATAAACA
Qy	6336	GGTTCCGGCGACATTTTCCCGAAAAAGTGCCACTGACGTC 6375
Db	6238	GGTTCCGGCGACATTTTCCCGAAAAAGTGCCACTGACGTC 6277

RESULT 13	EVP	CMV	PAL	6331 bp	DNA	linear	SYN
LOCUS	Expression vector	pCMV	PAL	for protein A fusions.			
DEFINITION	X96612						
ACCESSION	X96612.1	GI:1228975					
VERSION	expression vector; protein A.						
KEYWORDS	synthetic construct						
SOURCE	synthetic construct						
ORGANISM	artificial sequences.						
REFERENCE	1						
AUTHORS	Uetz, P. and Zeller, R.						
TITLE	Vectors for expression of protein-A-tagged proteins in						
JOURNAL	cells						
MEDLINE	Anal. Biochem. 237 (1), 161-163 (1996)						
PUBLISHED	96299083						
PURNED	8660557						
REFERENCE	2 (bases 1 to 6331)						
AUTHORS	Uetz, P. H.						
TITLE	Direct Submission						
JOURNAL	Submitted (07-MAR-1996) P. H. Uetz, EMBL, Differentiation						
MEYERHOESTR.	1, Heidelberg, 69117, FRG						
LOCATION/QUALIFIERS							
FEATURES	1..6331						
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gene	232..819						
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C#	G		
AU	E	a.	Site ID      Site      Score 3578.4; DB 12; Length 6331; Similarity 88.9%; Pred. No. 0; Conservative 0; Mismatches 16; Indels 503; Gaps 5;
Qy	Dt		175: GAGCTCAGCTTTTCGAGCGGGAAGAACCAGCTGGGGCTCTAGGGGGTATCCCCACGC 1809       214: GGCGTCTATGGCTTCGAGCGGGAAGAACCAGCTGGGGCTCTAGGGGGTATCCCCACGC 2200 
Qy	Dt		181: GCCCTGTAGCGGGCATTAAGCGCGGGGGTGTGGTGTTCAGCGGAGCGTAGCCGCTAC 1869 
Dt			220: GCCCTGTAGCGGGCATTAAGCGCGGGGGTGTGGTGTTCAGCGGAGCGTAGCCGCTAC 2260 
Qy	Dt		187: ACTTGCAGCGCCTACGCGCGCTCTCTTCGGCTTCTTCCTTCCCTTCTCGCACGACT 1929 
Dt			226: ACTTGCAGCGCCTACGCGCGCTCTCTTCGGCTTCTTCCTTCCCTTCTCGCACGACT 2320 
Qy	Dt		193: CGCGGGCTTCCCCTCAAGCTCTAAATCGGGG- TCCTTTTAGGGTTCCGATTAGTGC 1988 
Dt			232: CGCGGGCTTCCCCTCAAGCTCTAAATCGGGGCA TCCCTTTAGGGTTCCGATTAGTGC 2380 
Qy	Dt		198: TTACGGCAGCTCGACCCAAAAAACCTTGATTAGGGTGATGGTTCAAGTAGTGGGCCATC 2048 
Dt			238: TTACGGCAGCTCGACCCAAAAAACCTTGATTAGGGTGATGGTTCAAGTAGTGGGCCATC 2440 
Qy	Dt		204: CCCCTGATAGACGGTTTTTCGCCCTTTGACGCTCGAGTCCAGCTTCTTTAATAGTGACT 2108 
Dt			244: CCCCTGATAGACGGTTTTTCGCCCTTTTGAAGCTTGAAGTCCAGCTTCTTTAATAGTGACT 2500 
Qy	Dt		210: CTGTGTCAAAAC TGGAACAACACTCAACCCCTATCTCGGTCTATTCTTTTGATTTATAAGG 2168 
Dt			250: CTGTGTCAAAAC TGGAACAACACTCAACCCCTATCTCGGTCTATTCTTTTGATTTATAAGG 2560 
Qy	Dt		216: CATTTGCCGATTTCCGCGCTATTGGTTAAAAAATGAGCTGATTATAACAAAAATTTAAACGC 2228 
Dt			256: CATTTGCCGATTTCCGCGCTATTGGTTAAAAAATGAGCTGATTATAACAAAAATTTAAACGC 2620 

3335	3335	CGGCGCTTTCTGATTCATCGACTGTGGCGCGCTGTGGGTGGCGGACCGCTATCAG	Db	4312	TTTCCAGTCCGGAAACCTGTCTGTGCCAGCTGCATTAATGAATCGGCCAAACCGCG
3392	3692	TGGCCGCTTTTCTGGAATTCATCGACTGTGGCGCGCTGTGGGTGGCGGACCGCTATCAG	Qy	4416	AGGCGGTTTGGCTATTTGGGCGCTCTCTCGCTTCTCGCTCAGTCACTGACTCGCTGG
3395		CATAGCGTTGGCTTACCGGTGATATTCCTGAGAGCTTTGGCGGGAATGGCTGACCGC	Db	4372	AGGCGGTTTGGCTATTTGGGCGCTCTCTCGCTTCTCGCTCAGTCACTGACTCGCTGG
3752	3752	CATAGGTTTGGCTACCGGTGATATTCCTGAGAGCTTTGGCGGGAATGGCTGACCGC	Qy	4476	CGTTCCGGCTGCGCGGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATACGGTTATC
3455	3455	CCTCGCTTTTACCGGTATCGCGCTCCCAGATTCCGACGCGCATCGCTTCTATCGCTTT	Db	4432	CGTTCCGGCTGCGCGGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATACGGTTATC
3515	3515	TGACGAGTTCTTCTGAGCGGACTCTGGGGTTCGAATGACCGACCAACGACGCCCA	Qy	4536	ATCAGGGGNTAATCGCAGGAAGAACTGTGAGCAAAAGGCGGAGCAAAAGGCCAG
3872	3872	TGACGAGTTCTTCTGAGCGGACTCTGGGGTTCGAATGACCGACCAACGACGCCCA	Db	4492	ATCAGGGGNTAATCGCAGGAAGAACTGTGAGCAAAAGGCGGAGCAAAAGGCCAG
3575	3575	CTGCCATCAGGAGATTTTCGATTCCACCGCGCGCTTCTATGAAAGGTTGGGCTTCGAA	Qy	4596	TAAAGAGGCGCGGTTGTCTGGCGTTTTCATAGGCTCCGCCCCCTCTGACGAGCA
3882	3882	CTGCCATC-----	Db	4552	TAAAGAGGCGCGGTTGTCTGGCGTTTTCATAGGCTCCGCCCCCTCTGACGAGCA
3635	3635	GTTTTCCGGGACGCGCGCTGGATGATCTCCAGCGCGGGATCTCATGCTGGAGTTCT	Qy	4656	AAATCGACGCTCAAGTCAAGGTGCGGAAACCGCAGAGCACTATAAAGATAACA
3882	3882	-----	Db	4612	AAATCGACGCTCAAGTCAAGGTGCGGAAACCGCAGAGCACTATAAAGATAACA
3695	3695	GCCCCCTAGGGGAGGCTAACTGAACAACGAGAGGAGACAATACCGGAAGAACCC	Qy	4716	TCCCCCTGAGAGCTCCCTCGTGGCTCTCTGTTTCGAGCCCTGCGCCCTTACCGG
3882	3882	-----	Db	4672	TCCCCCTGAGAGCTCCCTCGTGGCTCTCTGTTTCGAGCCCTGCGCCCTTACCGG
3755	3755	GCATGACGGCAATAAAGACAGAAATAAAGCAAGCAAGTGTGGTGGTTTGTTCATAA	Qy	4776	GTCCGCCCTTCTCCCTTCCGGGAAGCGTGGCGCTTTCTCATAGCTCAACGCTGTAG
3882	3882	-----	Db	4732	GTCCGCCCTTCTCCCTTCCGGGAAGCGTGGCGCTTTCTCATAGCTCAACGCTGTAG
3815	3815	GCGGGTTCCGCTCCAGGCTGCACTCTGTGATACCCCAACCGAGACCCCATTTGGGG	Qy	4836	CAGTTCCGGGTAGGTTGGTTGGCTCCAAAGCTGGGCTGTGTGCAAGAACCCCGCT
3882	3882	-----	Db	4792	CAGTTCCGGGTAGGTTGGTTGGCTCCAAAGCTGGGCTGTGTGCAAGAACCCCGCT
3875	3875	AATA CGCGCGGTTTCTTCTTTTCCCCACCCCAACCCCAAGTTCCGGGTGAAGGCC	Qy	4896	CGACGCTGCGCTTTATCCGGTAACTATCGTCTTGAGTCCAAACCCCGGTAAAGACA
3882	3882	-----	Db	4852	CGACGCTGCGCTTTATCCGGTAACTATCGTCTTGAGTCCAAACCCCGGTAAAGACA
3935	3935	GGCTCGCAGCCAAAGTTCGGGGCGGAGGCCCTGCCATAGCTCAGTGTCTACGAGTTT	Qy	4956	ATCGCCACTGGCAGCAGCCACTGGTAAACGAGATTAGCAGAGCAGAGTATGTAGG
3891	3891	-----ACGAGATTT	Db	4912	ATCGCCACTGGCAGCAGCCACTGGTAAACGAGATTAGCAGAGCAGAGTATGTAGG
3995	3995	ATTCCACGCGCCTTCTATGAAAGTTGGGCTTCGGAATCGTTTCCGGGACGCGG	Qy	5016	TACAGAGTTCTTGAAGTGGTGGCTAACTATCGGCTACACTAGAAGAACAGTATT
3951	3951	ATTCCACGCGCCTTCTATGAAAGTTGGGCTTCGGAATCGTTTCCGGGACGCGG	Db	4972	TACAGAGTTCTTGAAGTGGTGGCTTAACTATCGGCTACACTAGAAGAACAGTATT
4055	4055	GGATGATCCTCAGCGCGGGATCTCATGCTGGAGTTCTTCGCGCACCCCAACTTGT	Qy	5076	CTGCGCTCTGCTGAAGCCAGTTTACCTTCGGAAGAAAGAGTTGTGTCTTGATC
4011	4011	GGATGATCCTCAGCGCGGGATCTCATGCTGGAGTTCTTCGCGCACCCCAACTTGT	Db	5032	CTGCGCTCTGCTGAAGCCAGTTTACCTTCGGAAGAAAGAGTTGTGTCTTGATC
4115	4115	TTGCACTTATAATGGTTACAAATAAGCAATAGCATCAAAATTTCAAAATAAAGC	Qy	5136	ACAAACCAACCGCTGTAGCGGTGGTTTGTGTTCGAGCAGCAGAGATTACCGG
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4175	4175	TTTTTTCATGTCATTTCTAGTTGGTTGTCCAAACTCATCAATGATCTTATCATGT	Qy	5196	AAAAGGATCTCAAGAAAGATCCCTTTGATCTTTTCTACCGGGTCTGACGCTCAGTG
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4235	4235	GTATACCGTTCGACCTCTAGCTAGAGCTGGCGTAACTCATGCTCATAGCTTTCCGT	Qy	5256	AAACTCAGTTTAAAGGATTTTGGTTCATGAGATTATCAAAAGGATCTTCAACCTA
4191	4191	GTATACCGTTCGACCTCTAGCTAGAGCTGGCGTAACTCATGCTCATAGCTTTCCGT	Db	5212	AAACTCAGTTTAAAGGATTTTGGTTCATGAGATTATCAAAAGGATCTTCAACCTA
4295	4295	3AAATGTATACCGCTCAAAATTCACAAATACGAGCCCGGAAGCAATAAGTGTAA	Qy	5316	TTTAAATTTAAATGAAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGG
4251	4251	3AAATGTATACCGCTCAAAATTCACAAATACGAGCCCGGAAGCAATAAGTGTAA	Db	5272	TTTAAATTTAAATGAAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGG
4355	4355	CCTGGGGTCAATGAGTGAGCTTAACATCAATTAATTTGGTTGGCTCACTGCCCGC	Qy	5376	CAGTTACCAATGCTTAATCAGTGGGACCTATCTCAGCGATCTCTCTATTTTGG
4311	4311	CCTGGGGTCAATGAGTGAGCTTAACATCAATTAATTTGGTTGGCTCACTGCCCGC	Db	5332	CAGTTACCAATGCTTAATCAGTGGGACCTATCTCAGCGATCTCTCTATTTTGG
4415	4415	TTCCAGTCCGGGAAACCTGTCTGCCAGCTGCAATTAATGAATCCGCCAAACCGCGGGAG	Qy	5436	CATAGTTCCGCTGCACTCCCGCTCGTGTAGTAATCACTACGATACCGGAGGGCTTAC

339: CATAGTTGCTGACTCCCGTCTGTAGATACATACATACGAGGGCTTACCATCTGG 5451  
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345: CCACAGTGTGCAATGATACCGGAGACCCACAGCTCACCGGCTCCAGATTATCAGCAAT 5511  
355: AACACAGCCAGCCGGAAGCCGAGCGCAGAGTGTCTGCAACTTTATTCGCGCTCCAT 5615  
351: AACACAGCCAGCCGGAAGCCGAGCGCAGAGTGTCTGCAACTTTATTCGCGCTCCAT 5571  
361: CAGTCTATTATTGTTGCGGGAAGCTAGAGTAAGTGTCCAGTGTAAATGTTGGG 5675  
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363: CAGTGTGTTGCAATGCTACAGGCACTGCTGTGTGTCAGCGTCTGTTGGTATGCGCTTC 5691  
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369: ATCAGTCTGCTTCCCAAGCATCAGGCGAGTTACATGATCCCATGTTGTGCAAAA 5751  
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375: ACGGTTAGTCTCTCGTCTCCGATCGTTGTGCAAGTAAGTGTGCGCGAGTGTATC 5811  
385: ATCATGTTATGCGAGCACTGCATATCTCTTACTGTGTCATGCCATCCGTAAAGTCTT 5915  
381: ATCATGTTATGCGAGCACTGCATATCTCTTACTGTGTCATGCCATCCGTAAAGTCTT 5871  
391: TCTGTGATGCTGTGAGTACTCAACAGTCAATCTGAGATAGTGTATGCGGCGAGGAG 5975  
387: TCTGTGATGCTGTGAGTACTCAACAGTCAATCTGAGATAGTGTATGCGGCGAGGAG 5931  
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393: TCTGTCTTGGCGGCTCAATACGGGCAATATACCGGCCACATAGCAGAACTTTAAAGT 5991  
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399: GTCATCATGGAAGAGTCTTCTGCGGCGGAAACTCTCAAGGATCTTACCGCTGTGAG 6051  
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AUTHORS Uetz,P. and Zeller,R.  
TITLE Vectors for expression of protein-A-tagged proteins in vertebrate cells  
JOURNAL Anal. Biochem. 237 (1), 161-163 (1996)  
MEDLINE 9629083  
PUBMED 8660557  
REFERENCE 2 (bases 1 to 6333)  
AUTHORS Uetz,P.H.  
TITLE Direct Submission  
JOURNAL Submitted (07-MAR-1996) P.H. Uetz, EMBL, Differentiation Biology Group, Meyerhofstr. 1, Heidelberg, 69117, FRG  
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ATTACCAATGCTTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCTGTTTCATC 5435  
ATTACCAATGCTTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCTGTTTCATC 5395  
TAGTTGCCCTGACTCCCGTCTGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGG 5495  
TAGTTGCCCTGACTCCCGTCTGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGG 5455  
CCAGTGCTCAATGATACCGCAGACCCACGCTCAACCGCTCCAGATTATACAGCAAT 5555  
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AGTCTATTAAATTTGTCGGGGAAGCTAGAGTAAGTGGTCCGCAATTAATAGTTTGGC 5675  
AGTCTATTAAATTTGTCGGGGAAGCTAGAGTAAGTGGTCCGCAATTAATAGTTTGGC 5635  
ACGTTGTTGCCATTCGTACAGGATCGTGGTCTCAGCTCGTCTGTTGGTATGGCTTC 5735  
ACGTTGTTGCCATTCGTACAGGATCGTGGTCTCAGCTCGTCTGTTGGTATGGCTTC 5695  
TCAGCTCCGGTTCCCAACGATCAAGCGAGTTACATGATCCCCCATGTTGTGCAAAA 5795  
TCAGCTCCGGTTCCCAACGATCAAGCGAGTTACATGATCCCCCATGTTGTGCAAAA 5755  
CGGTTAGCTCCTTCGGTCTCCGATCGTTGTGAGAAAGTAAAGTTGGCCGAGTGTATC 5855  
CGGTTAGCTCCTTCGGTCTCCGATCGTTGTGAGAAAGTAAAGTTGGCCGAGTGTATC 5815  
TCATGTTATGGCAGCAGTGCATAATCTTCTTACTGTATGATCCATCCGTAAGATGCTT 5915  
TCATGTTATGGCAGCAGTGCATAATCTTCTTACTGTATGATCCATCCGTAAGATGCTT 5875  
CTGTGACTGGTGAGTACTCAACCAAGTCACTCTGAGAAATAGTGTATGGGCGACCGAG 5975  
CTGTGACTGGTGAGTACTCAACCAAGTCACTCTGAGAAATAGTGTATGGGCGACCGAG 5935  
SCTCTTGCCGGCGGTCAATACGGGATTAATACCGCGCCACATAGCAGAACTTTAAAAGT 6035  
SCTCTTGCCGGCGGTCAATACGGGATTAATACCGCGCCACATAGCAGAACTTTAAAAGT 5995  
TCATCAATGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAG 6095  
TCATCAATGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAG 6055  
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CAGTTTCGATGTAAACCACTCGTGCAACCACTGATCTTCAGCATCTTTTACTTTTAC 6115  
CGGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCGCAAAAAGGGAATAAGGC 6215  
CGGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCGCAAAAAGGGAATAAGGC 6175  
CAGGAAATGTTGAATCTCATCTCTCTTTTCAATATTTATGAAGCATTTATCA 6275  
CAGGAAATGTTGAATCTCATCTCTCTTTTCAATATTTATGAAGCATTTATCA 6235

Qy 6276 GGGTTATTGTCTCATGAGCGGATACATATTTTGAATGTATTTAGAAAATAAACA  
Db 6236 GGGTTATTGTCTCATGAGCGGATACATATTTTGAATGTATTTAGAAAATAAACA  
Qy 6336 GGTTCGCGCACATTTTCCCGAAAAGTGCACACCTGACGTC 6375  
Db 6296 GGTTCGCGCACATTTTCCCGAAAAGTGCACACCTGACGTC 6335

Search completed: July 15, 2004, 15:25:47  
Job time : 23848 secs

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OM n: - nucleic search, using sw model

Run: July 15, 2004, 07:08:15 ; Search time 2170 seconds  
(without alignments)  
12480.305 Million cell updates/sec

File: US-10-668-496-2

Sequence: 6375  
1 GACGGATCGGAGATCTGGC.....GAAAGTCCACCTGACGTC 6375

Score: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Score: 3373863 seqs, 2124099041 residues

Total: number of hits satisfying chosen parameters: 6747726

Statistics: length: 0

Statistics: length: 200000000

Statistics: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Data:
- 1: N Geneseq\_29Jan04:\*
  - 1: Geneseqn1980s:\*
  - 2: Geneseqn1990s:\*
  - 3: Geneseqn2000s:\*
  - 4: Geneseqn2001as:\*
  - 5: Geneseqn2001bs:\*
  - 6: Geneseqn2002s:\*
  - 7: Geneseqn2003as:\*
  - 8: Geneseqn2003bs:\*
  - 9: Geneseqn2003cs:\*
  - 10: Geneseqn2004s:\*

1.0 is the number of results predicted by chance to have a  
ratio greater than or equal to the score of the result being printed,  
is derived by analysis of the total score distribution.

SUMMARIES

Record	Query	Match	Length	DB	ID	Description
581	56.2	6431	8	ACF57107		AcF57107 pCDNA3.1
582	56.2	7648	4	AAH48763		AAH48763 Vector pH
583	56.2	5653	2	AAT02998		AAT02998 RSV Car R
584	56.2	5900	6	ABQ81146		ABQ81146 Expressio
585	56.1	6216	2	AAV01425		AAV01425 Plasmid p
586	56.1	5431	6	ABN86685		ABN86685 Nucleotid
587	56.1	5431	9	ADE21866		ADE21866 Plasmid v
588	56.1	5432	3	AAZ89476		AAZ89476 Transgeni
589	56.1	5446	6	AAV38297		AAV38297 Plasmid p
590	56.1	5446	6	AAH18619		AAH18619 Renilla l
591	56.1	5446	6	ABL53540		ABL53540 Vector pc
592	56.1	6082	7	AAD56212		AAD56212 Human AB-
593	56.1	6082	7	AAD56211		AAD56211 Human AB-
594	56.1	6082	7	AAD56210		AAD56210 Human AB-
595	56.1	6085	7	AAD56213		AAD56213 Human PSM
596	56.1	6094	7	AAD56215		AAD56215 Human AB-
597	56.1	6100	6	ABK96469		ABK96469 Plasmid p
598	56.1	6135	6	ABK96470		ABK96470 Plasmid p
599	56.1	6180	4	AAD13062		AAD13062 pCDNA3-B1
600	56.1	6195	6	ABK51585		ABK51585 Nuclear t
601	56.1	6221	6	ABN86691		ABN86691 Nucleotid
602	56.1	6221	9	ADE21867		ADE21867 Plasmid v

24	3578.4	56.1	6238	2	AAV14339	AAV14339 Plasmid p
25	3578.4	56.1	6238	6	ABK51576	ABK51576 Nuclear t
26	3578.4	56.1	6338	2	AAT91384	AAT91384 RSV Car R
27	3578.4	56.1	6338	2	AAZ30851	AAZ30851 Expressio
28	3578.4	56.1	6338	3	AAZ87246	AAZ87246 Plasmid p
29	3578.4	56.1	6340	4	AAD13071	AAD13071 Plasmid p
30	3578.4	56.1	6411	4	AAD13063	AAD13063 Plasmid p
31	3578.4	56.1	6411	4	AAD13067	AAD13067 Plasmid p
32	3578.4	56.1	6436	4	AAD13078	AAD13078 Plasmid p
33	3578.4	56.1	6459	4	AAD13087	AAD13087 Plasmid p
34	3578.4	56.1	6459	4	AAD13093	AAD13093 Plasmid p
35	3578.4	56.1	6498	9	AAZ62465	AAZ62465 Plasmid p
36	3578.4	56.1	6582	9	AAZ62466	AAZ62466 Plasmid p
37	3578.4	56.1	6595	9	AAZ62471	AAZ62471 Plasmid p
38	3578.4	56.1	6607	4	AAD13072	AAD13072 Plasmid p
39	3578.4	56.1	6678	4	AAD13064	AAD13064 Plasmid p
40	3578.4	56.1	6703	4	AAD13079	AAD13079 Plasmid p
41	3578.4	56.1	6726	4	AAD13088	AAD13088 Plasmid p
42	3578.4	56.1	6727	4	AAD13094	AAD13094 Plasmid p
43	3578.4	56.1	6850	4	AAD13073	AAD13073 Plasmid p
44	3578.4	56.1	6921	4	AAD13065	AAD13065 Plasmid p
45	3578.4	56.1	6946	4	AAD13080	AAD13080 Plasmid p

ALIGNMENTS

RESULT 1	
ACF57107	
ID	ACF57107 standard; DNA; 6431 BP.
XX	
AC	ACF57107;
XX	
DT	14-OCT-2003 (first entry)
XX	
DE	pCDNA3.1(+)-Edg5 nucleotide sequence SEQ ID NO:4.
XX	
KW	Human; sphingosine 1 phosphate receptor; EDG5; CAM; identificat
KW	endothelial differentiation gene 5; constitutively active mutant
KW	ds.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO2003057882-A1.
XX	
PD	17-JUL-2003.
XX	
PF	07-JAN-2003; 2003WO-EF000070.
XX	
PR	12-JAN-2002; 2002EP-00000733.
XX	
PA	(AVET ) AVENTIS PHARMA DEUT GMBH.
XX	
PI	Fraissignes P, Gratzner S, Leberer E;
XX	
DR	WPI; 2003-577526/54.
XX	
PT	Identifying protein constitutively active mutants (CAMs) for id
PT	agonists or inverse agonists by transforming yeast cells with a
PT	of generated mutated sequences of a protein and identifying the
PT	respective protein CAM.
XX	
PS	Disclosure; Page 24-30; 46pp; English.
XX	
CC	The present invention describes a method for identifying protei
CC	constitutively active mutants (CAMs). The method comprises: (a)
CC	generating a library of mutated sequences of a protein; (b) trans
CC	yeast calls with the library; and (c) identifying the respective
CC	CAM. The method is useful for identifying agonists or inverse a
CC	The present sequence represents a human sphingosine 1 phosphate
CC	EDG5 (endothelial differentiation gene 5) related nucleotide se
CC	which is given in the exemplification of the present invention

31 BP; 1408 A; 1759 C; 1660 G; 1604 T; 0 U; 0 Other;

ilarity 56.2%; Score 3581.4; DB 8; Length 6431;  
Conservative 88.9%; Pred. No. 0;  
0; Mismatches 11; Indels 505;

Conservative 0; Mismatches 11; Indels 505; Gaps 5;

GCTCCAGCTTTTCTGAGGCGGAAGAACACGCTGGGGCTCTAGGGGGTATCCCCACGC 1809

GCTCTATGGCTTCTGAGCGGAAAGAACAGCTGGGGCTTAGGGGTATCCCCACGC 2304

CCTGTAGCGGGCGCATTAAGCGCGGGGTGTGGTTACGCCGACGGTGACCGCTAC 1869

CCTGTAGCGGCGCATTAAGCGCGCGGTGTGGTTACGCGCAGCGTGACCGCTAC 2364

TTGCCAGCGCCCTAGCGCCGCTCCTTTCGCTTCTTCCCTTCTCTGCGCCACGTT 1929

TTGCCAGCGCCCTAGCGCCGCTCTTTGGCTTCTTCCCTTCTTCCGCGCACTT 2424

CCGGCTTTTCCCGCTCAAGCTCTAAATC-GGGGCTCCCTTTAGGTTCCGATTTAGTGC 1988

CCGGCTTTTCCCCCGTCAAGCTCTATAATCGGGGGCTCCCTTTTAGGGTTCCGATTTTAGTGC 2484

TACGGACCTCGACCCCAAAAACCTTCAATTACCGCTCAATCGCTTTCACCTACGCTCCCAATC

[illegible]

**Figure 1**

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

[illegible][illegible]

**CONFIDENTIAL**

[illegible]

.....

[illegible]

2/33

JGC GGAAGAGAACAGCTGTGGAAATGGTGTACGTTAGGGTGTGGAAAGTCCCCAGGCT 23480

-----CTGTGGGAATGTGTGTTCAGTTAGGGTGTGGAAAGTCCCCAGGCT 2776

CCAGCAGGCAGGAAGTATGCCAAAGCATGCACTCTCAATTAGTCAGCAACCCAGGTGTGGAA 2408

CCAGCAGGCAGAGTATGCAAGCATGGATCTCAATTAGTCAGCAACCAGGTGTGGAA 2836

1CCCCAGGCTCCCCAGCAGGCAGAAGTATGCCAAGCATGTCATCTCAATTAGTCAGCAA 2468

TCCCCAGGCTCCCCAGCAGGCGAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAA 2896

ATAGTCCCGGCCCTAACTCCGGCCCATCCGGCCCTAACTCCGGCCAGTTCGGCCCAT 2528

ATAGTCCCGCCCCCTAACTCCGGCCCATCCCCGCCCTAACTCCGGCCAGTTCGGCCATT 2956

CGCCCCATGGCTGACTAATTATTTTATTTATGACAGGCCGAGGCCGCTCGGCCT 2588

CCGCCCATGGCTGACTAAATTTTATTTATGAGAGGCCGAGGCCCTCTGCCT 3016

3AGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTTGGAGGCCCTAGGCTTTTGGCAAAGATC 2648

3AGCTATTCAGAAGTAGTGAGGAGGCTTTTGTGGAGGCCCTAGGCTTTTGCAAAAGC 3076

-----GATCAAGAGACAGGATGAGGATCGTTTC 2676

CGGGAGCTTGTATATCCATTTTCGGATCTGATCAAGAGACAGGATGAGGATCGTTTC 3136

ATGATTTGAAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTAT 2736

3137	GCATGATTGAACAAGATAGGATTTGCACGAGGTTCTCCGGCCGCTGTGGTGGAGAC	Db
2737	TCGGCTATGACTCGGGCAACAAGACAATCGGCTGCTCTGATGCGCGCGTGTGCC	Qy
3197	TCGGCTATGACTCGGGCAACAAGACAATCGGCTGCTCTGATGCGCGCGTGTGCC	Db
2797	CAGCGCAGGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCTCGA	Qy
3257	CAGCGCAGGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCTCGA	Db
2857	TGCAAGACGAGCGCAGCGCGCTATCGTGGCTTGGCCACGACGGCGGTTCTTTGCG	Qy
3317	TGCAGGACGAGCGCAGCGCGCTATCGTGGCTTGGCCACGACGGCGGTTCTTTGCG	Db
2917	TGCTCGACGTTGTCTCACTGAAGCGGGAAGGACATGGGCTGTATTGGGCGAAGTGC	Qy
3377	TGCTCGACGTTGTCTCACTGAAGCGGGAAGGACATGGGCTGTATTGGGCGAAGTGC	Db
2977	AGGATCTCTGTCTCATCTCACCTTGCTCTCCGACGAAAGTATCCATCTATGGCTG	Qy
3437	AGGATCTCTGTCTCATCTCACCTTGCTCTCCGACGAAAGTATCCATCTATGGCTG	Db
3037	TGCGCGGCTGTCATACCGCTTTGATCCGCTACTTCGCCCATTCGACCAACCAAGCGA	Qy
3497	TGCGCGGCTGTCATACCGCTTTGATCCGCTACTTCGCCCATTCGACCAACCAAGCGA	Db
3097	GCATCGAGCGAGCAGCTACTCGGATGGAGCGGCTCTGTTCGATCAGGATGATCTC	Qy
3557	GCATCGAGCGAGCAGCTACTCGGATGGAGCGGCTCTGTTCGATCAGGATGATCTC	Db
3157	AAGAGCATACAGGGGCTCGCGCCAGCCGAACTGTTTCGCAGGCTCAAGGCGGACCA	Qy
3617	AAGAGCATACAGGGGCTCGCGCCAGCCGAACTGTTTCGCAGGCTCAAGGCGGACCA	Db
3217	ACGGCGAGGATCTCGTCTGTGACCCATGGCGATGCTGCTTGGCGGAATATCATGG	Qy
3677	ACGGCGAGGATCTCGTCTGTGACCCATGGCGATGCTGCTTGGCGGAATATCATGG	Db
3277	ATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCT	Qy
3737	ATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCT	Db
3337	ACATAGCGTTGGCTACCCGTTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTG	Qy
3797	ACATAGCGTTGGCTACCCGTTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTG	Db
3397	TCCTCGTGCTTTAAGGTATCGCGCTCCGATTCGACGCGCATCGCTTCTATCTC	Qy
3857	TCCTCGTGCTTTAAGGTATCGCGCTCCGATTCGACGCGCATCGCTTCTATCTC	Db
3457	TTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTTGGAAATGACCGCACCAAGCGAC	Qy
3917	TTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTTGGAAATGACCGCACCAAGCGAC	Db
3517	CTCTGCGCATCAGGATTTTCGATTCACCGCGCGCTTCTATGAAGGTGGGGCTTT	Qy
3977	CTCTGCGCATCAGGATTTTCGATTCACCGCGCGCTTCTATGAAGGTGGGGCTTT	Db
3577	CGTTTTCCGGGACCGCCGGCTGGATGATCTCTCAGCGCGGGATCTCATGCTCGAG	Qy
3986	-----	Db
3637	CGGCCACCTTAGGGGGAGGCTAATCTGAAACAACGGAAGGAGACAATACCGGAAGG	Qy
3986	-----	Db
3697	CGCATGACGCAATAAAGACAGAGATAAACGACGGTGTGGGTCTGTTTGTCT	Qy
3986	-----	Db
3757	CGCGGGGTTTGGTCCAGGGCTGGCACTCTGTTCGATACCCCAACGAGAGACCCCAT	Qy
3986	-----	Db

Q3	392	CAATACCCCGCGTTTCTTCTCTTTTCCCAACCCACCCCGCTTGGGTGAAGGCCCA	3976
D1	3980	-----	3985
Q3	397	GCGCTCGCAGCAACGTCCGGCGCGCAGGCCCTGCCATAGCCTCAGTGTACGAGATTTC	3936
D1	3986	-----ACAGATTTC	3995
Q3	393	GATTCCACCGCGCTTCTATGAAGAGTTGGGCTTCGGAATCGTTTTCGGGACGCGGC	3996
D1	3990	GATTCCACCGCGCTTCTATGAAGAGTTGGGCTTCGGAATCGTTTTCGGGACGCGGC	4055
Q3	399	TGGATGATCTCCAGCGGGGATCTCATGCTGGAGTTCTTCGCCCAACCCCACTTGT	4056
D1	405	TGGATGATCTCCAGCGGGGATCTCATGCTGGAGTTCTTCGCCCAACCCCACTTGT	4115
Q3	405	AATGCAGCTTATATGGTTACAATAAGCAATAGCATCAAAATTCACAAATAAGCA	4116
D1	411	AATGCAGCTTATATGGTTACAATAAGCAATAGCATCAAAATTCACAAATAAGCA	4175
Q3	411	TTTTTCCTAGCATTCATAGTTGGTTTGCACAACTCAATCAATATCTTATCATGTC	4176
D1	4174	TTTTTTCCTAGCATTCATAGTTGGTTTGCACAACTCAATCAATATCTTATCATGTC	4235
Q3	417	TGTATACCGTCGACCTCTAGCTAGAGCTTCGGCGTAATCATGTGTCATAGCTTGTTCCTGTG	4236
D1	4234	TGTATACCGTCGACCTCTAGCTAGAGCTTCGGCGTAATCATGTGTCATAGCTTGTTCCTGTG	4295
Q3	423	TGAAATGTTATTCGGCTCACAATTCACAAACATACGAGCCGGAAGCATAAAGTGTA	4296
D1	4290	TGAAATGTTATTCGGCTCACAATTCACAAACATACGAGCCGGAAGCATAAAGTGTA	4355
Q3	429	GCTCGGGTGCTTAATGAGTGAGCTAACTACATTAATTCGGTTGGCTCACTGCGCGT	4356
D1	4350	GCTCGGGTGCTTAATGAGTGAGCTAACTACATTAATTCGGTTGGCTCACTGCGCGT	4415
Q3	435	TTCAGTTCGGGAACCTGTGTGCGAGCTGCAATTAATGAATCGGCCAAGCGCGGGAGA	4416
D1	441	TTCAGTTCGGGAACCTGTGTGCGAGCTGCAATTAATGAATCGGCCAAGCGCGGGAGA	4475
Q3	441	GCGGTTTGCGTATTTGGCGCTCTTCGGCTTCCTCGCTCACTGCTGCGCTCGGTC	4476
D1	4470	GCGGTTTGCGTATTTGGCGCTCTTCGGCTTCCTCGCTCACTGCTGCGCTCGGTC	4535
Q3	447	GTTTCGGCTCGGCGAGCGGTATCAGCTCACTCAAAGCGGTATACGGTTATCCACGAA	4536
D1	453	GTTTCGGCTCGGCGAGCGGTATCAGCTCACTCAAAGCGGTATACGGTTATCCACGAA	4595
Q3	453	TACGGGATTAACGACGAAAGAACATGTGAGCAAAAGCCAGCAAAAGGCCAGAACCGT	4596
D1	4590	TACGGGATTAACGACGAAAGAACATGTGAGCAAAAGCCAGCAAAAGGCCAGAACCGT	4655
Q3	459	AAAGGCGCGTTGCTGGCGTTTTCATAGGCTCCGCCCTGACGAGCATCAAA	4656
D1	465	AAAGGCGCGTTGCTGGCGTTTTCATAGGCTCCGCCCTGACGAGCATCAAA	4715
Q3	465	AATCGACGCTCAAGTCAAGGTGCGGAAACCCGACAGACTATAAGATACCCAGGCGTT	4716
D1	471	AATCGACGCTCAAGTCAAGGTGCGGAAACCCGACAGACTATAAGATACCCAGGCGTT	4775
Q3	471	CCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTG	4776
D1	477	CCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTG	4835
Q3	477	TCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGTCAACGCTGTAGGTATCTC	4836
D1	483	TCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGTCAACGCTGTAGGTATCTC	4895
Q3	483	AGTTCCGCTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGCAAGAACCCCGGTCAGCC	4896
D1	489	AGTTCCGCTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGCAAGAACCCCGGTCAGCC	4955

Qy	4897	GACCGCTGCGCCCTTATCCCGTAACTATCGTCTTGAGTCCAAACCGGTAAGACAC	4956
Db	4956	GACCGCTGCGCCCTTATCCCGTAACTATCGTCTTGAGTCCAAACCGGTAAGACAC	5015
Qy	4957	TCGCCACTGCGCAGCAGCCACTCGGTAAACAGGATTAGCAGACGAGGATGTAGGC	5016
Db	5016	TCGCCACTGCGCAGCAGCCACTCGGTAAACAGGATTAGCAGACGAGGATGTAGGC	5075
Qy	5017	ACAGAGTTCTTGAAGTGGTGGCCCTAACTACGGCTACACTAGAGAAACAGTATT	5076
Db	5076	ACAGAGTTCTTGAAGTGGTGGCCCTAACTACGGCTACACTAGAGAAACAGTATT	5135
Qy	5077	TGGCTCTGCTGTAAGCCAGTTACCTTCGGAAAAAGAGTTCGTAGCTCTTGATCC	5136
Db	5136	TGGCTCTGCTGTAAGCCAGTTACCTTCGGAAAAAGAGTTCGTAGCTCTTGATCC	5195
Qy	5137	CAAAACCAACCGCTGGTAGCGGTGTTTTTTTTTTTGGTTCAGCAGCAGATTACGCGC	5196
Db	5196	CAAAACCAACCGCTGGTAGC---GGTTTTTTTTTTGCAAGCAGCAGATTACGCGC	5255
Qy	5197	AAAGGATCTCAAGAGATCCCTTTGATCTTTTCTACCGGGTCTGACGCTCAGTGC	5256
Db	5253	AAAGGATCTCAAGAGATCCCTTTGATCTTTTCTACCGGGTCTGACGCTCAGTGC	5312
Qy	5257	AACCTCAGCTTAAAGGGATTTTTGGTCATGAGATTATCAAAAAAGATCTTTCACCTAC	5313
Db	5313	AACCTCAGCTTAAAGGATTTTTGGTCATGAGATTATCAAAAAAGATCTTTCACCTAC	5372
Qy	5317	TTAAATTTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGC	5373
Db	5373	TTAAATTTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGC	5432
Qy	5377	AGTTACCAATGCTTAATCAGTGAAGGACCTATCTCAGCGATCTGTCTATTTCGT	5436
Db	5433	AGTTACCAATGCTTAATCAGTGAAGGACCTATCTCAGCGATCTGTCTATTTCGT	5492
Qy	5437	ATAGTTGCCCTGACTCCCGCTGCTGTAGATAAATCAAGATACGGAGGGCTTACCF	5496
Db	5493	ATAGTTGCCCTGACTCCCGCTGCTGTAGATAAATCAAGATACGGAGGGCTTACCF	5552
Qy	5497	CCAGTCTGCAATGATACCGCAGACCCACGCTCACCGCTCCAGATTTATCF	5556
Db	5553	CCAGTCTGCAATGATACCGCAGACCCACGCTCACCGCTCCAGATTTATCF	5612
Qy	5557	AACCAGCCAGCCGAAGGGCGAGCGAGAAGTGGTCTCTCAACTTTTATCCGCC	5616
Db	5613	AACCAGCCAGCCGAAGGGCGAGCGAGAAGTGGTCTCTCAACTTTTATCCGCC	5672
Qy	5617	CAGTCTAATTAATTTGTCGGGAGCTAGAGTAAGTAGTTGCGCAGTTAATAGT	5676
Db	5673	CAGTCTAATTAATTTGTCGGGAGCTAGAGTAAGTAGTTGCGCAGTTAATAGT	5732
Qy	5677	AACGTTCTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCTGTTGGTATC	5736
Db	5733	AACGTTCTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCTGTTGGTATC	5792
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Db	5793	TTACGCTCCGGTTCCCAACGATCAAGCGCAGTTACATGATCCGCCATGTTGTGC	5852
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Qy	5857	CTCATGTTTATGGCAGCACTGCATAATTCCTTACTGTCTATGCCATCCGTAAGA	5916
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RESULT 3  
AA020298  
ID AAT020298 standard; DNA; 5653 BP.  
XX AC AAT020298;  
XX DT 24-MAR-1996 (first entry)  
XX DE RSV tar Rev M10 expression plasmid pRSVRevM10.  
XX KW Plasmid pRSVRevM10; particle-mediated gene transfer; cyclic;  
KW particle acceleration; HIV virus infection; gene therapy; ss.  
XX OS Synthetic.  
XX FH  
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PE	XX		QY	2262	TATCCATTTTCGGATCTGATCAGCATGAGCGGGAAGAACCCAG-----CTGTGG	2317
PF	XX		DB	1908	TTTGGGGCTTTTCTGATTATCAACCGGGGTGAGTACCGAGCTCGAATTCGTGTGG	1967
PG	XX		QY	2318	TGTCAAGTTAGGGTGTGGAAAGTCCCGAGGCTCCCA-GCAGGCAGAAGTATGCA	2376
PH	XX		DB	1968	TGTCAAGTTAGGGTGTGGAAAGTCCCGAGGCTCCCGAGGCAGGAGAAGTATGCA	2027
PI	XX		QY	2377	GCATCTCAATTAGTCAGCAACCAAGGTGTGGAAAGTCCCGAGGCTCCCGAGCAGG	2436
PI	XX		DB	2028	GCATCTCAATTAGTCAGCAACCAAGGTGTGGAAAGTCCCGAGGCTCCCGAGCAGG	2087
PI	XX		QY	2437	TATGCAACATGATCTCAATTAGTCAGCAACCAAGTTCGGCCGCTTACCTCC	2496
PI	XX		DB	2088	TATGCAACATGATCTCAATTAGTCAGCAACCAAGTTCGGCCGCTTACCTCC	2147
PI	XX		QY	2497	CCCGCCCTTAATCTCCGCCAGTTCCGCCCATTTCTCGCCCATGCTGCTGACTAA	2556
PI	XX		DB	2148	CCCGCCCTTAATCTCCGCCAGTTCCGCCCATTTCTCGCCCATGCTGCTGACTAA	2207
PI	XX		QY	2557	TATTTATGAGAGGCGGAGCGGCTTCGGCTCTGAGCTATTCAGAAAGTAGTC	2616
PI	XX		DB	2208	TATTTATGAGAGGCGGAGCGGCTTCGGCTCTGAGCTATTCAGAAAGTAGTC	2267
PI	XX		QY	2617	CTTTTTCGAGCGCTAGGCTTTTGCNAAGATC-----	2648
PI	XX		DB	2268	CTTTTTCGAGCGCTAGGCTTTTGCNAAGATC-----	2327
PI	XX		QY	2649	----GATCAAGAGACAGGATGAGGATCGTTTCGCATGATTCGAACAGATGAT	2704
PI	XX		DB	2328	ATCTGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTCGAACAGATGAT	2387
PI	XX		QY	2705	AGTTTCTCCGGCGCTTGGTGAGAGGCTATTGGCTATGACTGGGCAACA	2764
PI	XX		DB	2388	AGTTTCTCCGGCGCTTGGTGAGAGGCTATTGGCTATGACTGGGCAACA	2447
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PI	XX		DB	2448	CGGCTGCTGATGCGCGCGTGTTCGGCTGTTCAGCGAGGGGCGCGCGTCT	2507
PI	XX		QY	2825	CAAGCCGACCTGTTCGGTGCGCTGAAATGAACTGCAAGACGAGGCAAGCGGCT	2884
PI	XX		DB	2508	CAAGCCGACCTGTTCGGTGCGCTGAAATGAACTGCAAGACGAGGCAAGCGGCT	2567
PI	XX		QY	2885	GCTGGCCACGACGGGCTTCTTGGCGAGCTGTGCTCGAGCTGTGCTCACTGAAGC	2944
PI	XX		DB	2568	GCTGGCCACGACGGGCTTCTTGGCGAGCTGTGCTCGAGCTGTGCTCACTGAAGC	2627
PI	XX		QY	2945	GGACTGGCTGCTATTGGGGGAGTCCGGGGCAGGATCTCTGCTCATCTCACT	3004
PI	XX		DB	2628	GGACTGGCTGCTATTGGGGGAGTCCGGGGCAGGATCTCTGCTCATCTCACT	2687
PI	XX		QY	3005	TGCGGAGAAAGTATCCATCATGCTGATGCAATTCGGCGGCTGCTGATCGCTTGA	3064
PI	XX		DB	2688	TGCGGAGAAAGTATCCATCATGCTGATGCAATTCGGCGGCTGCTGATCGCTTGA	2747
PI	XX		QY	3065	TACCTGCCCATTCGACACCAAGCGAAACATCGCATTCGAGCGAGCAGTACTCG	3124
PI	XX		DB	2748	TACCTGCCCATTCGACACCAAGCGAAACATCGCATTCGAGCGAGCAGTACTCG	2807
PI	XX		QY	3125	AGCGGCTCTTGTGATCAGATGATCTGCAAGAGGATCAGGGGCTCGCGC	3184
PI	XX		DB	2808	AGCGGCTCTTGTGATCAGATGATCTGCAAGAGGATCAGGGGCTCGCGC	2867
PI	XX		QY	3185	ACTGTTTCGCGAGGCTCAAGCGGAGATGCCGACGGCGAGGATCTCGTCTGTAC	3244
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Db 3603 TCATTAATTTGGCTTGGCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCGT  
Qy 4385 TGCAATTAATGAATCGGCAAAAGCGCGCGGAGAGCGGTTTTCGCTATTTGGGCGCT  
Db 3663 TGCAATTAATGAATCGGCAAAAGCGCGCGGAGAGCGGTTTTCGCTATTTGGGCGCT  
Qy 4445 CTTCTCTCGCTCACTGACTCGCTTGGCTCGCTCGCTTGGCTCGGCGGAGCGGTAT  
Db 3723 CTTCTCTCGCTCACTGACTCGCTTGGCTCGCTCGCTTGGCTCGGCGGAGCGGTAT  
Qy 4505 ACTCAAAAGGCGGTAATACGGTTATCCACAGAAATCAGGGGATAACCGCAGGAAAGA  
Db 3783 ACTCAAAAGGCGGTAATACGGTTATCCACAGAAATCAGGGGATAACCGCAGGAAAGA  
Qy 4565 GAGCAAAAGGCGCAGCAAAAGCGCAGGAAACCGTAAAGAGCGCGCTTTCGCTGGCGT  
Db 3843 GAGCAAAAGGCGCAGCAAAAGCGCAGGAAACCGTAAAGAGCGCGCTTTCGCTGGCGT  
Qy 4625 ATAGGCTCCGCGCCCTGAGGAGCATCACAAATTCAGAAATTCAGCTCAAGTCAAGGT  
Db 3903 ATAGGCTCCGCGCCCTGAGGAGCATCACAAATTCAGAAATTCAGCTCAAGTCAAGGT  
Qy 4685 ACCCGACAGGACTATAAAGATACCGAGCGCTTTCGCCCTTGGAAAGCTCCCTCGTGC  
Db 3963 ACCCGACAGGACTATAAAGATACCGAGCGCTTTCGCCCTTGGAAAGCTCCCTCGTGC  
Qy 4745 CTGTTCCGACCTTCCGCTTACCGGATACCGGATACCGTTCGCGCTTTCCTCCCTCGGAA  
Db 4023 CTGTTCCGACCTTCCGCTTACCGGATACCGGATACCGTTCGCGCTTTCCTCCCTCGGAA  
Qy 4805 CGCTTCTCATAGCTACCGCTTGGTATCTCAGTTCGCTGAGTTCGCTGCTTCGCT  
Db 4083 CGCTTCTCATAGCTACCGCTTGGTATCTCAGTTCGCTGAGTTCGCTGCTTCGCT  
Qy 4865 TGGCTCTGTGTCACGAAACCCCGCTTTCAGCGCCGACCGCTTCGCTTATCCGCTA  
Db 4143 TGGCTCTGTGTCACGAAACCCCGCTTTCAGCGCCGACCGCTTCGCTTATCCGCTA  
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Db 4203 GTCTTGAGTCCAAACCCCGCTTTCAGCACTTATTCGCTTCGCTGAGCGCACTG  
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Db 4263 GGATTACGAGCGGAGTATGAGGCGGCTACAGAGTTCCTGAAAGTGGTGGC  
Qy 5045 ACAGCTACACTAGAGAAACGATTTGGTATCTGCTCTCTGCTGAAAGCTGCTTA  
Db 4323 ACAGCTACACTAGAGAAACGATTTGGTATCTGCTCTCTGCTGAAAGCTGCTTA  
Qy 5105 GAAAGAGGTTGGTGGTTCCTGATCCGCGGCAACCAACCAACCGCTGCTGAGCGGTG  
Db 4383 GAAAGAGGTTGGTGGTTCCTGATCCGCGGCAACCAACCAACCGCTGCTGAGCGGTG  
Qy 5165 TTGTTTCCAAAGCAGCAGATTCGCGCAGAAAGGATCTCAAGAGATTCCTT  
Db 4443 TTGTTTCCAAAGCAGCAGATTCGCGCAGAAAGGATCTCAAGAGATTCCTT  
Qy 5225 TTTCTAGCGGTCTGAGCGCTCAGTGGAAACGAAACCTCACGTTAAGGATTTGG  
Db 4503 TTTCTAGCGGTCTGAGCGCTCAGTGGAAACGAAACCTCACGTTAAGGATTTGG  
Qy 5285 GATTATCAAAAGGATCTTCACTGAGTTCCTTTTAAATTAATAAGTGAAGTTTA  
Db 4563 GATTATCAAAAGGATCTTCACTGAGTTCCTTTTAAATTAATAAGTGAAGTTTA  
Qy 5345 TCTAAAGTATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTGT  
Db 4623 TCTAAAGTATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTGT  
Qy 5405 CTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTCGCTGACTCCCGCTCG



and production of vaccines, and in the production of agents. (Updated on 29-AUG-2003 to standardise OS field)

00 BP; 1395 A; 1519 C; 1512 G; 1484 T; 0 U; 0 Other; 56.2%; Score 3590.2; DB 6; Length 5900; ilarity 88.6%; Pred. No. 0; Conservative 0; Mismatches 63; Indels 470; Gaps 7;

3CTCCAGCTTTCTGAGGCGGAAGAACACAGCTGGGGCTCTAGGGGGTATCCCGACGC 1809  
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3CTCTATGGCTTCTGAGCGGGAAGAACACAGCTGGGGCTCTGAGGGGGGATCCCGACGC 1674  
|||||  
CCTGTAGCGGCGCAATTAAAGCGCGCGGGTGTGGTGGTTAGCGCAGCGTACCGGTAC 1869  
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CCTGTAGCGGCGCAATTAAAGCGCGCGGGTGTGGTGGTTAGCGCAGCGTACCGGTAC 1734  
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TTGCCAGGCGCTAGCGCGCGCTCTCTTTGCGTTTCCTCTTCCTTTCTCGCCACGTT 1929  
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|||||  
CGGCTTTCCCGGTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTGC 1988  
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TCAAAAGCATGCATCTCAATTAGTCAGCAACCAAGTTCGCGCCCTTAACTCGCGCCAT 2394  
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TTTTTTCGAGGCGCTAGGCTTTTGCAAGATC----- 2648  
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TTTTTTCGAGGCGCTAGGCTTTTGCAAAAGCTCCCGGAGCTTGGATATCCATTTTCGG 2574  
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QY	2649	----	GATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGAT
DB	2575	ATCTGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGAT	
QY	2705	AGGTTCTCCGGCCGGCTTGGGTGAGAGGCTATTTCGGCTATGACTCGGCGACAACA	
DB	2635	AGGTTCTCCGGCCGGCTTGGGTGAGAGGCTATTTCGGCTATGACTCGGCGACAACA	
QY	2765	CGGCTGCTTGATGCGCGCGTGTTCGGGCTGTCAGCGCAGGGGCGCGCCGGTTCT	
DB	2695	CGGCTGCTTGATGCGCGCGTGTTCGGGCTGTCAGCGCAGGGGCGCGCCGGTTCT	
QY	2825	CAAGACCGACTGTTCGGGTGCTTGAACTGACGAGGAGGAGGCGCGCGGCT	
DB	2755	CAAGACCGACTGTTCGGGTGCTTGAACTGACGAGGAGGAGGCGCGCGGCT	
QY	2885	GCTGGCCACGACGGGGGCTTCCTTGGCGAGCTGTGCTGACGTTGTCTCACTGAAGC	
DB	2815	GCTGGCCACGACGGGGGCTTCCTTGGCGAGCTGTGCTGACGTTGTCTCACTGAAGC	
QY	2945	GGACTGGCTGCTATTGGGCGAGGTGCGGGGCGAGATCTCTGTGCATCTCACT	
DB	2875	GGACTGGCTGCTATTGGGCGAGGTGCGGGGCGAGATCTCTGTGCATCTCACT	
QY	3005	TGCCGGAAGATTCATCATGCTGCTGACGCTGCTGACGTTGTCTCACTGAAGC	
DB	2935	TGCCGGAAGATTCATCATGCTGCTGACGCTGCTGACGTTGTCTCACTGAAGC	
QY	3065	TACTGCGCCATTGACCAACCAAGCGAATCATCGCATCGAGCGAGCATCGTACTCG	
DB	2995	TACTGCGCCATTGACCAACCAAGCGAATCATCGCATCGAGCGAGCATCGTACTCG	
QY	3125	AGCGGCTGCTGATCGAGTGATCTGACGAGGAGCATGAGGGGCTCGCGCC	
DB	3055	AGCGGCTGCTGATCGAGTGATCTGACGAGGAGCATGAGGGGCTCGCGCC	
QY	3185	ACTGTTTCGCGAGGCTCAAGGCGAGCATGCGCGAGCGGCGAGGATCTCGCTGAGC	
DB	3115	ACTGTTTCGCGAGGCTCAAGGCGGCGATGCGCGAGCGGCGAGGATCTCGCTGAGC	
QY	3245	CGATGCTGCTTCGCGAATCATGCTGAGAAATGGCGGCTTTCTGGATTCTCAT	
DB	3175	CGATGCTGCTTCGCGAATCATGCTGAGAAATGGCGGCTTTCTGGATTCTCAT	
QY	3305	TGGCGGCTGGGTGGCGGACCGCTATCAGGACATAGCGTTGGGCTACCGGTGA	
DB	3235	TGGCGGCTGGGTGGCGGACCGCTATCAGGACATAGCGTTGGGCTACCGGTGA	
QY	3365	TGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGTGTCTTACGATACGC	
DB	3295	TGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGTGTCTTACGATACGC	
QY	3425	CGATTGCGGCGCATCGCTTCTATCGGCTTCTTGAAGGTTCTTCTGAGCGGG	
DB	3355	CGATTGCGGCGCATCGCTTCTATCGGCTTCTTGAAGGTTCTTCTGAGCGGG	
QY	3485	GGGTTGGAATGACCGAACGAGCGCCAACTTGCCATCAGAGATTTTCGAT	
DB	3415	GGGTTGGAATGACCGAACGAGCGCCAACTTGCCATCAGAGATTTTCGAT	
QY	3545	GCGGCTTCTATGAAGGTTGGGCTTCGGAATCGTTTTCGGGACGCGCGGCTGG	
DB	3456	-----	
QY	3605	CTCAGCGGGGATCTCATGCTGGAGTTCTTCGCCCACTAGGGGGAGGCTAT	
DB	3456	-----	
QY	3665	ACACGGAAGGACAAATACCGGAAGGACCCCGGCATGACGGCAATAAAGAGC	
DB	3456	-----	
QY	3725	AAACGCAACGCTGTGGTGGTTGTTTCAAAACGCGGGGTTTCGGTCCCGAGGCT	

1456 ----- 3455  
 1785 CTGTGATACCCACGAGACCCCAATTGGGGCCCAATACGCCCGGTTTCTTCTTTTCC 3844  
 1457 ----- 3455  
 1841 CAACCCCAACCCCAAGTTCCGGGTGAAGGCCACAGGGCTCGCAGCCAACTCGGGGGCGCAG 3904  
 1458 ----- 3455  
 1901 GGCCTGCCATAGCCTCAGTCTACGAGATTTGATTTCCACCGCGGCTTCTATGAAGGT 3964  
 1459 -----ACGAGATTTCCGATTTCCACCGCGGCTTCTATGAAGGT 3493  
 1961 TCGGGCTTCGGAATCGTTTTCCGGGACCGCGGCTGGATGATCTCTCCAGCGCGGGATCTCA 4024  
 1494 TCGGGCTTCGGAATCGTTTTCCGGGACCGCGGCTGGATGATCTCTCCAGCGCGGGATCTCA 3553  
 1021 TCGGTGAGTTCTTCGCCCAACCCCAACTTGTATTTCAGCTTATAATGGTTACAAATAAA 4084  
 1554 TCGGTGAGTTCTTCGCCCAACCCCAACTTGTATTTCAGCTTATAATGGTTACAAATAAA 3613  
 1061 GCAATAGCATCACAATTTTCAAAATAAAGCATTTTTTTCATGCAATCTAGTTGGTT 4144  
 1614 GCAATAGCATCACAATTTTCAAAATAAAGCATTTTTTTCATGCAATCTAGTTGGTT 3673  
 1141 TGTCCAAACTCATCAATGTATCTTATCATGTCTGTATACCGTCGACCTCTAGCTAGGCT 4204  
 1674 TGTCCAAACTCATCAATGTATCTTATCATGTCTGTATACCGTCGACCT-----CGAGGCT 3729  
 1201 TCGGTGAATCATGTCATAGCTGTTTCTGTGTGAATTTTATTCGCTCACAATTCAC 4264  
 1736 TCGGTGAATCATGTCATAGCTGTTTCTGTGTGAATTTTATTCGCTCACAATTCAC 3789  
 1261 AACATACGCGGAGCATTAAGGTAAAGCTTGGGCTGCTTAATGAGTGAGTAC 4324  
 1791 AACATACGCGGAGCATTAAGGTAAAGCTTGGGCTGCTTAATGAGTGAGTAC 3849  
 1321 TCACATTAATTGGTTTCGCTCACTCCCGCTTTCACATCGGGAACCTGTCTGTCAGC 4384  
 1851 TCACATTAATTGGTTTCGCTCACTCCCGCTTTCACATCGGGAACCTGTCTGTCAGC 3909  
 1381 TGCATTAATGAATTCGCCAAACGCGCGGGAGAGCGGTTTGGGTATTTGGCGCTTTCCG 4444  
 1911 TGCATTAATGAATTCGCCAAACGCGCGGGAGAGCGGTTTGGGTATTTGGCGCTTTCCG 3969  
 1441 CTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGGCGAGCGGTATCAGCTC 4504  
 1971 CTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGGTCGCGGAGCGGTATCAGCTC 4029  
 1501 AATCAAGCGGTAATACCGGTTATCCACAGAAATCAGGGGATACGAGGAAAGAAATGT 4564  
 1034 ACTCAAGCGGTAATACCGGTTATCCACAGAAATCAGGGGATACGAGGAAAGAAATGT 4089  
 1561 GAGCAAAAGCCGAGCAAAAGCCAGAAACGTTAAAGCGCGGTTGCTGGCGCTTTTCC 4624  
 1091 GAGCAAAAGCCGAGCAAAAGCCAGAAACGTTAAAGCGCGGTTGCTGGCGCTTTTCC 4149  
 1621 AATAGGCTTCGCGCCCTGACGAGCATCACAATAATCGAGCTCAAGTCAAGGTGCGAA 4684  
 1415 AATAGGCTTCGCGCCCTGACGAGCATCACAATAATCGAGCTCAAGTCAAGGTGCGAA 4209  
 1681 ACCGACAGGACTATAAGATACAGCGGTTTCCCGCTGGAAGCTCCCTCGTCGCTCTC 4744  
 121 ACCGACAGGACTATAAGATACAGCGGTTTCCCGCTGGAAGCTCCCTCGTCGCTCTC 4269  
 1741 CTGTTCCGACCTTCGCGCTTACCGGATACCTGTTCGCGCTTTCTCCCTTCGGGAAGCGTG 4804  
 1421 CTGTTCCGACCTTCGCGCTTACCGGATACCTGTTCGCGCTTTCTCCCTTCGGGAAGCGTG 4329  
 1801 CCGTTTCTCATAGCTCAGCGCTAGGATCTCATAGTTCCGTTGGTGTAGTCTCGTCCAGC 4864

4330 CGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCCGTTGAGTTCGTTGCT 4389  
 4865 TGGGCTGTGTGCACGAACCCCGGTTTACGCCGACCGCTGCGCTTATCCGGT 4924  
 4390 TGGGCTGTGTGCACGAACCCCGGTTTACGCCGACCGCTGCGCTTATCCGGT 4449  
 4925 GTCTTGAAGTCCAAACCGGTAAGACACGACTTATCGCACTTCGCGAGCAGCACTG 4974  
 4450 GTCTTGAAGTCCAAACCGGTAAGACACGACTTATCGCACTTCGCGAGCAGCACTG 4509  
 4985 GATTTAGCAGACGAGGATATGTAGCGGTGCTACAGAGTTCTTGAAGTGTGTC 5044  
 4510 GATTTAGCAGACGAGGATATGTAGCGGTGCTACAGAGTTCTTGAAGTGTGTC 4569  
 5045 ACGGCTTACACTAGAAAGACAGTATTGGTATCTCGCTCTGCTGAAGCCAGTTA 5104  
 4570 ACGGCTTACACTAGAAAGACAGTATTGGTATCTCGCTCTGCTGAAGCCAGTTA 4629  
 5105 GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCAGCTGTTGAGCGTG 5164  
 4630 GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCAGCTGTTGAGCGTG 4689  
 5165 TTGTTTGAAGCAGCAGATTAACCGCAGAAAAAAGGATCTCAAGAGATCCTT 5224  
 4690 TTGTTTGAAGCAGCAGATTAACCGCAGAAAAAAGGATCTCAAGAGATCCTT 4749  
 5225 TTTCTACGGGCTGTGACGCTCAGTGGAAACGAAACCTCAGCTTAAGGATTTTGG 5284  
 4750 TTTCTACGGGCTGTGACGCTCAGTGGAAACGAAACCTCAGCTTAAGGATTTTGG 4809  
 5285 GATTTCAAAAAGGATTTTCACTAGATCCTTTTAAATTTAAATGAAGTTT 5344  
 4810 GATTTCAAAAAGGATTTTCACTAGATCCTTTTAAATTTAAATGAAGTTT 4869  
 5345 TCTAAGTATATATGATTAACCTTGTCTGACAGTTTACCAATGCTTAACTCAGTG 5404  
 4870 TCTAAGTATATATGATTAACCTTGTCTGACAGTTTACCAATGCTTAACTCAGTG 4929  
 5405 CTATCTCAGCGATCTGTCTATTTCGTTTCATCATAGTTGCTGACCTCCCGCTG 5464  
 4930 CTATCTCAGCGATCTGTCTATTTCGTTTCATCATAGTTGCTGACCTCCCGCTG 4989  
 5465 TAACTACGATACGGGAGGCTTACCATCTGGCCCAAGTCTGCAATGATACCGC 5524  
 4990 TAACTACGATACGGGAGGCTTACCATCTGGCCCAAGTCTGCAATGATACCGC 5049  
 5525 CACGCTCACCGGCTCCAGATTTATCAGCAATAAACGACGACCGGAGGCGCG 5584  
 5050 CACGCTCACCGGCTCCAGATTTATCAGCAATAAACGACGACCGGAGGCGCG 5109  
 5585 GAAGTGGTCTCTGCAACTTTTATCCGCTCCATCCAGTCTATTAATTTGTCGCGG 5644  
 5110 GAAGTGGTCTCTGCAACTTTTATCCGCTCCATCCAGTCTATTAATTTGTCGCGG 5169  
 5645 GAGTAAAGTATGTCGCGAGTTAATAGTTTCCGCAACGTTGTCGCAATGCTCAAG 5704  
 5170 GAGTAAAGTATGTCGCGAGTTAATAGTTTCCGCAACGTTGTCGCAATGCTCAAG 5229  
 5705 TGGTGTACGCTCGCTGTTTGGTATGGCTTCAATCAGCTCCGCTCCCAACGAT 5764  
 5230 TGGTGTACGCTCGCTGTTTGGTATGGCTTCAATCAGCTCCGCTCCCAACGAT 5289  
 5765 GAGTTACATGATCCCGGCTGTTTGTGCAAAAAAGCGTTAGCTCTCTTTCGCTCCTC 5824  
 5290 GAGTTACATGATCCCGGCTGTTTGTGCAAAAAAGCGTTAGCTCTCTTTCGCTCCTC 5349  
 5825 TTGTGAGAGTAAAGTTGCGCGAGTGTATCACTCATGTTATGCGAGCACTGTC 5884  
 5350 TTGTGAGAGTAAAGTTGCGCGAGTGTATCACTCATGTTATGCGAGCACTGTC 5409  
 5885 CTCCTTACTGTGATCCATCCGATAGTGTCTTTCTGTGATGCTGCTGAGTACTCAA 5944  
 5410 CTCCTTACTGTGATCCATCCGATAGTGTCTTTCTGTGATGCTGCTGAGTACTCAA 5469

andard: DNA: 6216 BP.

/ASK8-SmGST3 DNA.

ccine; glutathione S-transferase; schistosomiasis; mansoni; blood fluke; ss.

1.

; 97WO-US003977.

; 96US-0013321P.

TH ALABAMA MEDICAL SCI FOUN.

**schistosomiasis - comprising a non-integrating DNA sequence histosoma mansonii glutathione S-transferase.**

p 7a; 57pp; English.

as been developed comprising a non-infectious, non-integrating DNA encoding *Schistosoma mansoni* glutathione S-transferase (GST) fused to a protein of interest. The GST gene is operably linked to a promoter. The present sequence is a GST gene fused to a protein of interest.

SQ Sequence 6216 BP; 1428 A; 1624 C; 1627 G; 1537 T; 0 U; 0 Other;  
Query Match 56.1%; Score 3578.6; DB 2; Length 6216;  
Best Local Similarity 88.6%; Pred. No. 0;  
Matches 4157; Conservative 0; Mismatches 64; Indels 470;

QY 1810 GCCCTGTAGCGGCGCATTAAGCGCGGGTGTGGTGTACCGCGCAGCGTGAC  
|||  
pb 1991 GCCCTGTAGCGGCGCATTAAGCGCGGGTGTGGTGTACCGCGCAGCGTGAC

Qy	1930	CGCGGGCTTCCCGTCAAGCTCTAAATCGGGC	-TCCCTTTAGGGTTCGGATT
pH	2.111	CGCGGGCTTCCCGTCAAGCTCTAAATCGGGC	CGCGGGCTTCCCGTCAAGCTCTAAATCGGGC

QY 2049 GCCTGTAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAG

QY 2169 GATTTTGGCGATTTCGGCGCTATTGGTTAAAAAATGAGCTGATTTTACAAAAATT

DD	2411	GAATTTTAAACAAATATATACGTTTACAATTTAAATATTGCTTATACAAATCT
QY	2262	TATCCATTTTCGGATCTGATCAGCACTGAGCGCGGAAGAACCGAG-----CTGTGG

DB	2531	TGTCAGTTAGGGTGTCGAATGTC	CCCCCAGGCTCCCCCAGGCGAGGATATGCT
QY	2377	GCATCTCAATTAGTCAGCAAC	CAGGTGTGGAAAGTCCCCCAGGCTCCCCCAGCAGG

Db	2651	TATGCAAGCATGTCATCTCAATTAGTCAGCAACCATAGTCCCGCCCTAACTCC
Qy	2497	CCCGGCCCTAACTCCGCCCAGTTCGGCCCATTTCTCGCCCCCATGGCTGACTAAT

Db	2771	TATTTATG	CAGAGG	CGCGCT	CTGGCC	TATTC	CAGAGT	AGT
Qy	2517	CTTTTTTT	TGGAGG	CC	TAGC	TTTTT	TGCAAG	ATC-----



283: CTTTTTGAGGCTAGGCTTTTGC AAAAAGCTCCCGGAGCTTGGATATCCATTTTCGG 2890  
 264: ---GATCAAGAGACAGGATGAGATCGTTTCGATGATGAACTGAACAAGATGGATTGCACGC 2704  
 289: ATCTGATCAAGAGACAGGATGAGATCGTTTCGATGATGAACTGAACAAGATGGATTGCACGC 2950  
 370: AGTTCTCCGGCGCTTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACAAGACAAT 2764  
 395: AGTTCTCCGGCGCTTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACAAGACAAT 3010  
 276: CGCTGCTCTGATCGCGCGTGTTCGGCTGTGACGCGAGGCGCGCTTTCTTTTGT 2824  
 301: CGCTGCTCTGATCGCGCGTGTTCGGCTGTGACGCGAGGCGCGCTTTCTTTTGT 3070  
 280: CAGACCGACCTGTCCGGTGCCCTGAATGAACCTGCAAGACGAGCGAGCGGCTATCGTG 2884  
 307: CAGACCGACCTGTCCGGTGCCCTGAATGAACCTGCAAGACGAGCGAGCGGCTATCGTG 3130  
 288: GTTGGCAAGACGCGGCTTCTTTCGAGCTGTGCTGAGCTGTGCTCACTGAAGCGGGAAG 2944  
 313: GTTGGCAAGACGCGGCTTCTTTCGAGCTGTGCTGAGCTGTGCTCACTGAAGCGGGAAG 3190  
 294: GAACTGGCTGTATTGGGCGAAGTGCAGGCGAGGATCTCTGTCTATCTCACTGCTGCC 3004  
 319: GAACTGGCTGTATTGGGCGAAGTGCAGGCGAGGATCTCTGTCTATCTCACTGCTGCC 3250  
 300: TCCGAGAAAGTATCCATCATGTGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGC 3064  
 325: TCCGAGAAAGTATCCATCATGTGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGC 3310  
 306: TACCTGCCATTCGACCAACAAGCGAAACATCGCATCGAGCGAGCAGTACTCGGATGA 3124  
 331: TACCTGCCATTCGACCAACAAGCGAAACATCGCATCGAGCGAGCAGTACTCGGATGA 3370  
 312: AGCGGCTTGTGATCAGATGATCTGACGAGAGATCTCGTGTGACCCATGG 3244  
 343: ACTGTTCCGACGCTCAGGCGGCTATGCCGAGGAGTCTCGTGTGACCCATGG 3490  
 324: CATGCTCTTGGCCGAATATCATGTGGAATAATGGCCGCTTTCTGGATTATCGACTG 3304  
 349: CATGCTCTTGGCCGAATATCATGTGGAATAATGGCCGCTTTCTGGATTATCGACTG 3350  
 330: TCGCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGGCTTGGCTACCGGTGATATGC 3364  
 355: TCGCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGGCTTGGCTACCGGTGATATGC 3610  
 336: TGAAGAGCTTGGCGGGAATGGGCTGACCGCTTCTCGTGTTCAGGATCGCCGCTCC 3424  
 361: TGAAGAGCTTGGCGGGAATGGGCTGACCGCTTCTCGTGTTCAGGATCGCCGCTCC 3670  
 342: CATTCGACGCGATCGCTTCTATCGCTTCTTGAAGTCTTCTGAGCGGGAATCTTG 3484  
 367: CATTCGACGCGATCGCTTCTATCGCTTCTTGAAGTCTTCTGAGCGGGAATCTTG 3730  
 348: GGTTCGAATGACCGACGAGCGGCGCAACCTGCGCATCAGGATTCGATTCACC 3544  
 373: GGTTCGAATGACCGACGAGCGGCGCAACCTGCGCATCAGGATTCGATTCACC 3771  
 354: CGCGCTTCTATGAAAGTTGGGCTTTCGGAATCGTTTTCGGGACGCGGCTGGATGATC 3604  
 377: ----- 3771  
 360: CTCAGCGCGGGAATCTCATGTGGAGTTCTTCGCCCAACCTTAGGGGAGGCTAACTGAA 3664  
 377: ----- 3771  
 366: AACGGAGGAGACAATACCGGAAGGNAACCGGCGCATGACGGCAATAAAAGACAGATA 3724

3772: ----- 3772  
 3725: AAACGACGGTGTGGGTCTGTTTGTATATAAACGGGGGTTCGGTCCAGGGCT 3784  
 3772: ----- 3771  
 3785: CTGTGATATACCCACGAGACCCCATTTGGGGCCAATACGCCCGGTTTCTTCT 3844  
 3772: ----- 3771  
 3845: CACCCACCCCAAGTTCCGGGTGAAGCCAGGGCTCGACGCAACGTCGGGG 3864  
 3772: ----- 3771  
 3905: GGCCTGCCATAGCTCAGTGTCTACGAGATTTCGATTCCACCGCGGCTTCTATG 3964  
 3772: -----ACGAGATTTCGATTCCACCGCGGCTTCTATG 3809  
 3965: TGGGCTTCGGAATCGTTTTCGCGGAGCGCGGCTGGATGATCTCCAGCGGGG 4024  
 3810: TGGGCTTCGGAATCGTTTTCGCGGAGCGCGGCTGGATGATCTCCAGCGGGG 3869  
 4025: TGTGAGGTTCTTCGCCACCCCACTTGTATTTCGAGCTTATATGTTTACA 4084  
 3870: TGTGAGGTTCTTCGCCACCCCACTTGTATTTCGAGCTTATATGTTTACA 3929  
 4085: GCAATAGCATCAAAATTTACAAATAAAGCATTTTTTTCACCTGCACTTAGTT 4144  
 3930: GCAATAGCATCAAAATTTACAAATAAAGCATTTTTTTCACCTGCACTTAGTT 3989  
 4145: TGTCCAACTCATCAATGATCTTATCATGTCTGTATACCGTCGACCTTAGCT 4204  
 3990: TGTCCAACTCATCAATGATCTTATCATGTCTGTATCCGATCCGTCGACCT 4045  
 4205: TGGGCTTAATCANGTTCATAGCTGTTTTCCTGTGTAATGTTTATCGCTCAG 4264  
 4046: TGGGCTTAATCANGTTCATAGCTGTTTTCCTGTGTAATGTTTATCGCTCAG 4105  
 4265: ACAACATACGAGCGGAAGCATAAAGTGTAAAGCCCTGGGGTGCCTAATGAGTGA 4324  
 4106: ACAACATACGAGCGGAAGCATAAAGTGTAAAGCCCTGGGGTGCCTAATGAGTGA 4165  
 4325: TCACATTAATTCGTTTTCGCTCACTGCCGCTTTTCAGTTCGGGAAACCTGTGCT 4384  
 4166: TCACATTAATTCGTTTTCGCTCACTGCCGCTTTTCAGTTCGGGAAACCTGTGCT 4225  
 4385: TGCATTAATGAAATCGGCCAAACGCGGGGAGAGGCGGTTTGGGTATTTGGCGCT 4444  
 4226: TGCATTAATGAAATCGGCCAAACGCGGGGAGAGGCGGTTTGGGTATTTGGCGCT 4285  
 4445: CTTCTCTCGCTCACTGACTCGCTCGCTCGCTCGCTTCGGTTCGGTTCGGGAGCGGTAT 4504  
 4286: CTTCTCTCGCTCACTGACTCGCTCGCTCGCTCGCTTCGGTTCGGTTCGGGAGCGGTAT 4345  
 4505: ACTCAAGCGGTAATACGTTTATCCACAGAAATCAGGGGATACCGAGGAAAGA 4564  
 4346: ACTCAAGCGGTAATACGTTTATCCACAGAAATCAGGGGATACCGAGGAAAGA 4405  
 4565: GAGCAAAAGCGCAGCAAAAGGCGAGCAACCGGTAAAGGCGCGTTTGGTGGCGT 4624  
 4406: GAGCAAAAGCGCAGCAAAAGGCGAGCAACCGGTAAAGGCGCGTTTGGTGGCGT 4465  
 4625: ATAGGCTCGCGCCCTCGACGAGCATCACAAAATTCGACGCTCAAGTCAGAGGT 4684  
 4466: ATAGGCTCGCGCCCTCGACGAGCATCACAAAATTCGACGCTCAAGTCAGAGGT 4525  
 4685: ACCGACAGGACTATAAGATACGAGGCGTTTCCCTCGGAAAGCTCCCTCGTGC 4744  
 4526: ACCGACAGGACTATAAGATACGAGGCGTTTCCCTCGGAAAGCTCCCTCGTGC 4585  
 4745: CTGTTCCGACCTCGGCTTACGGATACCTGTCGCGCTTTCTCCCTTCGGGAA 4804  
 4586: CTGTTCCGACCTCGGCTTACGGATACCTGTCGCGCTTTCTCCCTTCGGGAA 4645

CTTTCTCATAGCTCAGCGTGTAGGTATCTCAGTTGGTGTAGTGGTTCGCTCCAGC 4864  
CTTTCTCAATGCTCAGCGTGTAGGTATCTCAGTTGGTGTAGTGGTTCGCTCCAGC 4705  
GGCTGTGTGCAAGAACCCCGCTTCAGCCCGGACCGCTGGCTTATCCGGTAACTATC 4924  
GGCTGTGTGCAAGAACCCCGCTTCAGCCCGGACCGCTGGCTTATCCGGTAACTATC 4765  
CTTGAGTCCAAACCGGTAAAGACAGACTTATCGCACTGGCAGAGCCACTGGTAACA 4984  
CTTGAGTCCAAACCGGTAAAGACAGACTTATCGCACTGGCAGAGCCACTGGTAACA 4825  
ATTAGCAGAGCAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACT 5044  
ATTAGCAGAGCAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACT 4895  
GGCTACACTAGAAAGACAGTATTTGGTATCTGGCTCTGCTGAAGCCAGTTACCTTGG 5104  
GGCTACACTAGAAAGACAGTATTTGGTATCTGGCTCTGCTGAAGCCAGTTACCTTGG 4945  
AAAAGAGTTGGTGTAGCTTCTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGTTTT 5164  
AAAAGAGTTGGTGTAGCTTCTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGTTTT 5005  
GTTTGCAGCAGCAGATTAACGCGCAGAAAAAGGATCTCAAGAGATCCTTTGATCT 5224  
GTTTGCAGCAGCAGATTAACGCGCAGAAAAAGGATCTCAAGAGATCCTTTGATCT 5065  
TCTACGGGTCTGACGCTCAGTGGAAACGAAACTCAAGTTAAGGATTTTGGTCAATGA 5284  
TCTACGGGTCTGACGCTCAGTGGAAACGAAACTCAAGTTAAGGATTTTGGTCAATGA 5125  
TTATCAAAAGGATCTTACCTAGATCCTTTTAAATTAAGTTAAGTTTAAATCAA 5344  
TTATCAAAAGGATCTTACCTAGATCCTTTTAAATTAAGTTAAGTTTAAATCAA 5185  
TAAAGTATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTCAGGCAC 5404  
TAAAGTATATATAGTAAACTTGGTCTGACAGTTACCAATGCTTAAATCAGTCAGGCAC 5245  
ATCTCAGGATCTGTCTATTTGGTTCATCCTAGTGTGCTGACTCCCGCTGCTGAGA 5464  
ATCTCAGGATCTGTCTATTTGGTTCATCCTAGTGTGCTGACTCCCGCTGCTGAGA 5305  
ACTAGATACGGGAGGCTTACCATCTGGCCCGGCTGCTGCAATGATACCGGAGACC 5524  
ACTAGATACGGGAGGCTTACCATCTGGCCCGGCTGCTGCAATGATACCGGAGACC 5365  
CGCTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCCGAGGCGGCGCA 5584  
CGCTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCCGAGGCGGCGCA 5425  
AGTGGTCTGCAACTTTATCCGCTCCATCCAGTCTTAAATTTGGTGGCGGAAGCTA 5644  
AGTGGTCTGCAACTTTATCCGCTCCATCCAGTCTTAAATTTGGTGGCGGAAGCTA 5485  
GTAAGTGTTCGCCAGTTAATAGTTTGGCAACGTTTGGCCATTTGCTACAGGCATCG 5704  
GTAAGTGTTCGCCAGTTAATAGTTTGGCAACGTTTGGCCATTTGCTACAGGCATCG 5545  
GTGTCAAGTGTTCGCCAGTTAATAGTTTGGCAACGTTTGGCCATTTGCTACAGGCATCG 5764  
GTGTCAAGTGTTCGCCAGTTAATAGTTTGGCAACGTTTGGCCATTTGCTACAGGCATCG 5605  
GTTATGATCCCGCATGTTGGCAAAAGCGGTAGTCTCTTGGTCTCCGATCG 5824  
GTTATGATCCCGCATGTTGGCAAAAGCGGTAGTCTCTTGGTCTCCGATCG 5665  
GTGAGAGTAAGTTGGCCGAGTGTATCACTCATGTTTATGGCAGCACTGATTAATT 5884  
GTGAGAGTAAGTTGGCCGAGTGTATCACTCATGTTTATGGCAGCACTGATTAATT 5725

QY 5885 CTCTTACTGTCTATCCCATCGTAAGATGCTTTTCTGTGATGCTGTGAGTACTCA 5885  
Db 5726 CTCTTACTGTCTATCCCATCGTAAGATGCTTTTCTGTGATGCTGTGAGTACTCA 5726  
QY 5945 CATTTCTGAGATAGTGTATGCGGCGACCGAGTGTCTCTTGGCCCGGCTCAATAC 5945  
Db 5786 CATTTCTGAGATAGTGTATGCGGCGACCGAGTGTCTCTTGGCCCGGCTCAATAC 5786  
QY 6005 ATACCGCGCCACATAGCAGAACTTTTAAAGTGTCTCATCATTTGGAAAAAGTTCTT 6005  
Db 5846 ATACCGCGCCACATAGCAGAACTTTTAAAGTGTCTCATCATTTGGAAAAAGTTCTT 5846  
QY 6065 GAAATCTCTCAAGGATCTTACCGCTGTGAGATCCAGTTCCGATGTAAACCCACTC 6065  
Db 5906 GAAATCTCTCAAGGATCTTACCGCTGTGAGATCCAGTTCCGATGTAAACCCACTC 5906  
QY 6125 CCAACTGATCTTCAAGCATCTTTTACTTTTCAACAGCGTTTCTGGGTGAGCAAAA 6125  
Db 5966 CCAACTGATCTTCAAGCATCTTTTACTTTTCAACAGCGTTTCTGGGTGAGCAAAA 5966  
QY 6185 GGGAAATGCGCAAAAAAGGATTAAGGGGACACCGAAATGTGATTAATCTCA 6185  
Db 6026 GGGAAATGCGCAAAAAAGGATTAAGGGGACACCGAAATGTGATTAATCTCA 6026  
QY 6245 TCCTTTTCAATATTTTGAAGCATTTTATCAGGTTATTTGCTCATGAGCGGAT 6245  
Db 6086 TCCTTTTCAATATTTTGAAGCATTTTATCAGGTTATTTGCTCATGAGCGGAT 6086  
QY 6305 TTGAATGTATTTAGAAAAATAAACAATAGGGGTTCCGCGCACATTTCCCGGAA 6305  
Db 6146 TTGAATGTATTTAGAAAAATAAACAATAGGGGTTCCGCGCACATTTCCCGGAA 6146  
QY 6365 CACCTGAGTC 6375  
Db 6206 CACCTGAGTC 6216

RESULT 6

ABN86685  
ID ABN86685 standard; DNA; 5431 BP.  
XX AC ABN86685;  
XX AC  
DT 05-NOV-2002 (first entry)  
XX DE Nucleotide sequence of a pcDNA3 plasmid vector.  
XX DE Major histocompatibility complex; MHC; antigen presenting cell;  
XX KW antigen; cytostatic; virucide; gene therapy; CD8; vaccine; ther;  
XX KW cancer; viral infection; ds.  
XX OS Synthetic.  
XX PN WO200261113-A2.  
XX PD 08-AUG-2002.  
XX PP 01-FEB-2002; 2002WO-US0002598.  
XX PR 01-FEB-2001; 2001US-0265334P.  
XX PA (UJJO ) UNIV JOHNS HOPKINS.  
XX PI Wu T, Hung C;  
XX DR WPI; 2002-619261/66.  
XX PT Nucleic acid molecule encoding a fusion polypeptide that promot;  
XX PT processing via the Major Histocompatibility Complex class I pat;  
XX PT and/or promotes activity of an antigen presenting cell, useful;  
XX PT for cancer and viral infections.  
PS Claim 24; Page 22-23; 127pp; English.



[illegible]

QY	4656	AAATCGACGCTCAAGTCGAGAGGTGGCGAAACCCGACAGAGCTATATAAGATACCA
DB	3712	AAATCGACGCTCAAGTCGAGAGGTGGCGAAACCCGACAGAGCTATATAAGATACCA
QY	4716	TCCCCCTGGGAAGCTCCCTCGTGGCGCTCTCTGTTTCCGACCCCTCGCGCTTACCGG
DB	3772	TCCCCCTGGGAAGCTCCCTCGTGGCGCTCTCTGTTTCCGACCCCTCGCGCTTACCGG
QY	4776	GTCCGCCCTTCTCCCTTCGGGAAGCGTGGCGCTTTTCTCATAGCTCA CGCTGTATAG
DB	3832	GTCCGCCCTTCTCCCTTCGGGAAGCGTGGCGCTTTTCTCAATGCTCA CGCTGTATAG
QY	4836	CAGTTCCGGGTGAGTGCCTTCCCTCCAAAGCTGGCGCTGTGCGACGAAACCCCGCT
DB	3892	CAGTTCCGGGTGAGTGCCTTCCCTCCAAAGCTGGCGCTGTGCGACGAAACCCCGCT
QY	4896	CGACCGCTGCGCCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCCGTAAGACA
DB	3952	CGACCGCTGCGCCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCCGTAAGACA
QY	4956	ATCCGCCATCTGGCAGCAGCCACTGGTAAACAGATTTAGCAGACGAGGTA TGTAGG
DB	4012	ATCCGCCATCTGGCAGCAGCCACTGGTAAACAGATTTAGCAGACGAGGTA TGTAGG
QY	5016	TACAGAGTTCTTGAAGTGGTGGCTAACTACGCTACACTAGACGCTACACTAGAAGAACATGTT
DB	4072	TACAGAGTTCTTGAAGTGGTGGCTAACTACGCTACACTAGAAGAACATGTT
QY	5076	CTCGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTTGATCTC
DB	4132	CTCGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTTGATCTC
QY	5136	ACAAACCAACCGCTGGTAGCGGTGGTTTTTTTGTTCGACGACGACGATTAACGG
DB	4192	ACAAACCAACCGCTGGTAGCGGTGGTTTTTTTGTTCGACGACGACGATTAACGG
QY	5196	AAAAGGATCTCAAGAGATCTTTTGATCTTTTCTA CGGGCTCTGACGCTCAGTGTG
DB	4252	AAAAGGATCTCAAGAGATCTTTTGATCTTTTCTA CGGGCTCTGACGCTCAGTGTG
QY	5256	AAACTCAGGTTAAGGATTTTGGTCATGAGATTTATCAAAAAGGATCTTCACTCA
DB	4312	AAACTCAGGTTAAGGATTTTGGTCATGAGATTTATCAAAAAGGATCTTCACTCA
QY	5316	TTTAAATTTAAAAATGAAGTTTAAATCAATCTCAAAAGTATATATAGTAAACTTG
DB	4372	TTTAAATTTAAAAATGAAGTTTAAATCAATCTAAAGTATATATAGTAAACTTG
QY	5376	CAGTTACCAATGCTTAATCAAGTAGGCACTATCTCAGCGATCTGTCTATTTCCG
DB	4432	CAGTTACCAATGCTTAATCAAGTAGGCACTATCTCAGCGATCTGTCTATTTCCG
QY	5436	CATAGTTGCCCTGACTCCCGCTCGTGTAGATAA CTACGATACGGGAGGGCTTAC
DB	4492	CATAGTTGCCCTGACTCCCGCTCGTGTAGATAA CTACGATACGGGAGGGCTTAC
QY	5496	CCCCAGTGTGCAATGATACCGCGAGACCAACCGCTCAACCGGCTCCAGATTTATC
DB	4552	CCCCAGTGTGCAATGATACCGCGAGACCAACCGCTCAACCGGCTCCAGATTTATC
QY	5556	AAACCAAGCCAGCCGGAAGGGCCGAGCGCAGAGTGTCTGTGAACTTTATCCGCG
DB	4612	AAACCAAGCCAGCCGGAAGGGCCGAGCGCAGAGTGTCTGTGAACTTTATCCGCG
QY	5616	CCAGTCTATTAAATTTGTTCCGGGAAGCTAGAGTAAAGTAGTTCCGCCAGTTAAATAG
DB	4672	CCAGTCTATTAAATTTGTTCCGGGAAGCTAGAGTAAAGTAGTTCCGCCAGTTAAATAG
QY	5676	CAACGTTGTTGCCATTGCTACAGGCATCTGTGTGTCAACGCTCGTCTGTTGGTATN
DB	4732	CAACGTTGTTGCCATTGCTACAGGCATCTGTGTGTCAACGCTCGTCTGTTGGTATN
QY	5736	ATTCAAGCTCCGGTTCCCAACGATCAAGGGCGAGTTTACATGATCCCGCAATGTGTG

[illegible]

	New nucleic acid encoding a chimeric fusion or fusion polypeptide comprising a first domain with a translocation polypeptide, and a second domain with an antigen having at least one antigenic peptide, useful for treating cancer.
XX	Disclosure; SEQ ID NO 8; 69pp; English.
PS	The present invention describes a nucleic acid (I) encoding a c fusion or fusion polypeptide comprising a first domain with a translocation polypeptide, and a second domain comprising an antigen having at least one antigenic peptide. Also described: (1) an expression vector comprising (I) operatively linked to a promoter and operator in a cell; (2) a particle comprising (I) or the expression vector; (3) a cell that has been modified to comprise (I) or the expression vector; (4) a chimeric polypeptide comprising a first domain with a translocation polypeptide, and a second domain comprising an antigen having at least one antigenic peptide; (5) a pharmaceutical composition capable of inducing or enhancing an antigen specific immune response, comprising (I), expression vector, particle, cell, cell of the particle, or the chimeric polypeptide; and a carrier or excipient; (6) increasing an antigen specific immune response by administering the composition described above; (7) increasing the number of CD8 + T cells specific for a selected desired antigen in a subject by administering the composition described above; and (8) inhibiting the growth of a tumor in a subject by administering the composition described above. (I) has cytostatic activity, and can be used in immunotherapy, and gene therapy. The nucleic acids (I), compositions and methods are useful for treating cancer. The present sequence represents a plasmid vector nucleic acid sequence which is used in the exemplification of the present invention.
XX	
SQ	Sequence 5431 BP; 1253 A; 1413 C; 1386 G; 1379 T; 0 U; 0 Other;
Query Match	56.1%; Score 3578.4; DB 9; Length 5431;
Best Local Similarity	88.9%; Pred. No. 0;
Matches 4141; Conservative	0; Mismatches 16; Indels 503; Nups 5;
QY	1750 GAGCTCAGGTTTTCGAGCGGAAGAACCAGCTGGGCTTAGGGGTATCC
DB	1241 GGCTCTATGGCTTCTGAGCGGAAGAACCAGCTGGGCTTAGGGGTATCC
QY	1810 GCCTGTAGCGGGCATTAAGCGCGCGGTGTGGTGTACCGCAGCGTGAC
DB	1301 GCCTGTAGCGGGCATTAAGCGCGCGGTGTGGTGTACCGCAGCGTGAC
QY	1870 ACTTGCAGCGCCCTAGCGCCGCTCTTTTCGCTTCTTCCCTCTCTTCGCG
DB	1361 ACTTGCAGCGCCCTAGCGCCGCTCTTTTCGCTTCTTCCCTCTCTTCGCG
QY	1930 CGCGCGCTTTCGCCGTCAGCTCTAAATCGGGC-TCCCTTTAGGGTCCGATT
DB	1421 CGCGCGCTTTCGCCGTCAGCTCTAAATCGGGCACTCCCTTTAGGGTCCGATT
QY	1989 TTTCAGGCACCTCGACCCCAAATAAATCTGATTAGGGTGATGTTTCACGTAGTC
DB	1481 TTTCAGGCACCTCGACCCCAAATAAATCTGATTAGGGTGATGTTTCACGTAGTC
QY	2049 GCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCAAGTTCTTTAATAG
DB	1541 GCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCAAGTTCTTTAATAG
QY	2109 CTGTGTTCCAAACTGGAAACAACACTCAACCTACTCGGTCTATTCTTTTCATT
DB	1601 CTGTGTTCCAAACTGGAAACAACACTCAACCTACTCGGTCTATTCTTTTCATT
QY	2169 GAATTTTCCGCAATTCGGCCCTATTGGTTAAAAAATAGCTGATTTAACAAAAAT
DB	1661 GAATTTTGGGATTTCCGCCCTATTGGTTAAAAAATAGCTGATTTAACAAAAAT
QY	2229 GAATTAATCTGTGGAAATGCCCGGAGCTTGTATATCCATTTTCGATCTGATC
DB	1721 GAATTAAT-----









Q3 3274 AATGGCGGCTTTCTCGATTATCGACTGTGGCGGCTGGTGTGGGACCGCTATCAG 3335  
D2 3275 AATGGCGGCTTTCTCGATTATCGACTGTGGCGGCTGGTGTGGGACCGCTATCAG 3336  
Q3 3336 GACATAGCGTTGGCTACCGCTGATATTTGCTGAAGAGCTTGGCGGCGAATGGCGCTGACCGC 3395  
D2 3337 GACATAGCGTTGGCTACCGCTGATATTTGCTGAAGAGCTTGGCGGCGAATGGCGCTGACCGC 3396  
Q3 3397 CCTCGTCTTTACGGTATCGCGCTCCGATTCGACGGCATCGCTTTCTATCGCTTT 3455  
D2 3398 CCTCGTCTTTACGGTATCGCGCTCCGATTCGACGGCATCGCTTTCTATCGCTTT 3456  
Q3 3457 CTGACGAGCTTTCTGACGGGACTCTGGGGTTGCAATATGACCGACCGACCGCCCA 3515  
D2 3458 CTGACGAGCTTTCTGACGGGACTCTGGGGTTGCAATATGACCGACCGACCGCCCA 3516  
Q3 3517 ACCTGCGCATCACGAGATTTGATTCACCGCGCGCTTCTATGAAGTGGTTCGGAA 3575  
D2 3518 ACCTGCGCATC----- 3576  
Q3 3577 CTGTTTTCGGGACGCGGCTGGATGATCTCCAGCGCGGGATCTCATGCTGGAGTTCT 3635  
D2 3578 CTGTTTTCGGGACGCGGCTGGATGATCTCCAGCGCGGGATCTCATGCTGGAGTTCT 3636  
Q3 3637 TGCCCACTTAGGGGAGCTTAATGAAACACGGAAGGAGACAATACCGAAGGAACCC 3695  
D2 3638 TGCCCACTTAGGGGAGCTTAATGAAACACGGAAGGAGACAATACCGAAGGAACCC 3696  
Q3 3697 GCGCATGACGGCAATAAAGAAGACAGAAACGACAGCTGTGGGTTCGTTGTCATAA 3755  
D2 3698 GCGCATGACGGCAATAAAGAAGACAGAAACGACAGCTGTGGGTTCGTTGTCATAA 3756  
Q3 3757 ACGCGGGGTTGCTCCAGGCTGGCACTCTGTGCGATACCCACGAGACCCCAATTGGG 3815  
D2 3758 ACGCGGGGTTGCTCCAGGCTGGCACTCTGTGCGATACCCACGAGACCCCAATTGGG 3816  
Q3 3817 CCAATAGCGCGGTTTCTCTTTTCCCAACCCACCCCAAGTTCGGGTGAAGGCC 3875  
D2 3818 CCAATAGCGCGGTTTCTCTTTTCCCAACCCACCCCAAGTTCGGGTGAAGGCC 3876  
Q3 3877 AAGGCTCGCAGCAACAGCTCGGGCGGAGCGCTGCCATAGCTCAGTGTACGAGATTT 3935  
D2 3878 AAGGCTCGCAGCAACAGCTCGGGCGGAGCGCTGCCATAGCTCAGTGTACGAGATTT 3936  
Q3 3937 CATTCACCGCGGCTTTCTATGAAGAGTTGGCTTCGAAATCGTTTTCGGGACCGCG 3995  
D2 3938 CATTCACCGCGGCTTTCTATGAAGAGTTGGCTTCGAAATCGTTTTCGGGACCGCG 3996  
Q3 3997 CCGATGATCTCCAGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCAACTTGT 4055  
D2 3998 CCGATGATCTCCAGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCAACTTGT 4056  
Q3 4057 CCGATGATCTCCAGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCAACTTGT 4112  
D2 4058 CCGATGATCTCCAGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCAACTTGT 4113  
Q3 4117 TATTCAGCTTATATGTTTACAAATAAGCAATAGCATCACAAATTTACAAATAAGC 4175  
D2 4118 TATTCAGCTTATATGTTTACAAATAAGCAATAGCATCACAAATTTACAAATAAGC 4176  
Q3 4177 ATTTTTCATGCACTCTAGTTGGTTTTCGAAATCTCATCAATGATCTTATCATGT 4235  
D2 4178 ATTTTTCATGCACTCTAGTTGGTTTTCGAAATCTCATCAATGATCTTATCATGT 4236  
Q3 4237 CCGATACCGTCTAGCTTAGAGTTGGGTAATCATGCTCATGCTTCTCTGT 4295  
D2 4238 CCGATACCGTCTAGCTTAGAGTTGGGTAATCATGCTCATGCTTCTCTGT 4296  
Q3 4297 GCGAATTTGTTATCCGCTCACAAATCCACACATACGACCGGAAGCATAAAGTGTA 4355  
D2 4298 GCGAATTTGTTATCCGCTCACAAATCCACACATACGACCGGAAGCATAAAGTGTA 4356  
Q3 4357 AGCTGGGTTGCTTAATGAGTGAAGTAACTCATATTAATGCGTTCGCTCATGCGCG 4415  
D2 4358 AGCTGGGTTGCTTAATGAGTGAAGTAACTCATATTAATGCGTTCGCTCATGCGCG 4416  
Q3 4417 TTCCAGTCCGGAAACCTGTCTGCGCAGCTGCATTAATGAATCGGCCAACGCGCGGAG 4475  
D2 4418 TTCCAGTCCGGAAACCTGTCTGCGCAGCTGCATTAATGAATCGGCCAACGCGCGGAG 4476

3413 TTTCCAGTCCGGAAACCTGTCTGCGCAGCTGCATTAATGAATCGGCCAACCGCG 3472  
4416 AGCGGTTTGGCTATTTGGGCGCTCTTCCGCTTCTCGCTCCTGCTCAGTACGCTGCG 4475  
3473 AGCGGTTTGGCTATTTGGGCGCTCTTCCGCTTCTCGCTCCTGCTCAGTACGCTGCG 3532  
4476 CGTTCCGCTGCGCGCAGCGGATTCAGCTCAGTCAAAAGCGGTAATACGGTTATC 4535  
3533 CGTTCCGCTGCGCGCAGCGGATTCAGCTCAGTCAAAAGCGGTAATACGGTTATC 3592  
4536 ATCAGGGGATTAACGCGAAGAAACATGTGAGCAAAAGCCAGCAAAAGCCAG 4595  
3593 ATCAGGGGATTAACGCGAAGAAACATGTGAGCAAAAGCCAGCAAAAGCCAG 3652  
4596 TAAAGGCGGCTTCTGCTGCGCTTTTCCATAGGCTCCGCCCTCGACGAGCA 4655  
3653 TAAAGGCGGCTTCTGCTGCGCTTTTCCATAGGCTCCGCCCTCGACGAGCA 3712  
4656 AAATCGACGCTCAAGTTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCA 4715  
3713 AAATCGACGCTCAAGTTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCA 3772  
4716 TCCCTCGTGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTGCGCGCTTACCG 4775  
3773 TCCCTCGTGAAGCTCCCTCGTGGCTCTCTCTGTTCCGACCTGCGCGCTTACCG 3832  
4776 GTCCGCTTCTTCCCTTCGGGAAGCTGGCGCTTTCTCATAGCTCAGCTACGCTAG 4835  
3833 GTCCGCTTCTTCCCTTCGGGAAGCTGGCGCTTTCTCATAGCTCAGCTAGCTAG 3892  
4836 CAGTTTGGTGTAGTGTGTTTCCCTTCCAGCTGGGCTGTGTGACGAAACCCCGCT 4895  
3893 CAGTTTGGTGTAGTGTGTTTCCCTTCCAGCTGGGCTGTGTGACGAAACCCCGCT 3952  
4896 CGACGCTGCGCTTATCCGCTTAACTATCTGTTGAGTCTCAACCCCGGTAAGACA 4955  
3953 CGACGCTGCGCTTATCCGCTTAACTATCTGTTGAGTCTCAACCCCGGTAAGACA 4012  
4956 ATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTTAGCAGAGCAGGATGTAG 5015  
4013 ATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTTAGCAGAGCAGGATGTAG 4072  
5016 TACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTACACTAGAAGAACAGTAT 5075  
4073 TACAGAGTTCTTGAAGTGGTGGCTTAACTACGGCTACACTAGAAGAACAGTAT 4132  
5076 CTGCGCTCTGCTGAAGCAGTTACCTTCGGAAGAGAGTTGGTAGCTCTTGATC 5135  
4133 CTGCGCTCTGCTGAAGCAGTTACCTTCGGAAGAGAGTTGGTAGCTCTTGATC 4192  
5136 ACAACCCAGCTGGTAGCGGTGTTTCTTGTTCGAAAGCAGCAGATTTACCGG 5195  
4193 ACAACCCAGCTGGTAGCGGTGTTTCTTGTTCGAAAGCAGCAGATTTACCGG 4252  
5196 AAAAGATCTCAAGAGATCTTGTGATCTTCTACGGGGTCTGACGCTCAGTG 5255  
4253 AAAAGATCTCAAGAGATCTTGTGATCTTCTACGGGGTCTGACGCTCAGTG 4312  
5256 AAATCAGCTTAAAGGATTTTGGTTCATGAGATTTCAAAAGAGATCTTCACTTA 5315  
4313 AAATCAGCTTAAAGGATTTTGGTTCATGAGATTTCAAAAGAGATCTTCACTTA 4372  
5316 TTTAAATTTAAATGAAGTTTAAATCAATCAATCAATCAATCAATCAATCAATCA 5375  
4373 TTTAAATTTAAATGAAGTTTAAATCAATCAATCAATCAATCAATCAATCAATCA 4432  
5376 CAGTTTCCAAATGCTTAAATCAGTGAGGACCTATCTCAGCGATCTGTCTATTTCG 5435  
4433 CAGTTTCCAAATGCTTAAATCAGTGAGGACCTATCTCAGCGATCTGTCTATTTCG 4492  
5436 CATAGTTGCTGCTACCTCCCGCTGCTGTAGTAACTACGATACGGGAGGCTTACC 5495

NA3.



|||||  
TTTTTTCATCTGCAATTCTAGTTGTGGTTTTGTCCAAACTCATCAATGTATCTTATCATGT 3246  
  
GTATACCGTTCGACCTCTAGCTAGAGCTTGCGCGTAATCATGTGCATAGCTGTGTTCTCTGT 4235  
  
GTATACCGTTCGACCTCTAGCTAGAGCTTGCGCGTAATCATGTGCATAGCTGTGTTCTCTGT 3306  
  
GAATAATTGTATTCGGCTCACAATTCACACAAATACGAGCCGGAAGCATAAAGTGTAA 4295  
GAATAATTGTATTCGGCTCACAATTCACACAAATACGAGCCGGAAGCATAAAGTGTAA 3366  
  
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CTCGGGTGCCTAATGAGTAGAGCTAACCTCACATTAATTCGGTTGCGTCACTGCCCGC 3426  
  
TCCAGTCGGGAAACCCTGTCGTGCCAGCTGCATTAATGAATTCGCCCAACCGCGCGGGAG 4415  
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ACCGCTGCGCCTTATCCGGTAACTATCGTCTCAGTCCAAACCCGGTAAGACACGACTT 4955  
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CAGAGTTCTTTGAAGTGGTGCCTTAACTACGGCTACACTAGGAAGAACAGTATTTGGTAT 4146  
  
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CGGCTCTGCTGAAGCCAGTTACTCTTCGGA AAAAGAGTTGGTAGCTTTGATCCGGCAA 4206  
  
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AAACCAACCGCTGGTAGGGTGGTTTTTTGTTTTGCAAGCAGCAGATTACGGCGAGAA 4266  
  
AAGGATCTCAAGAAAGATCCCTTTGATCTTTTTCTACGGGGTCTGACGCTCAGTGGAAACGA 5255

4267 AAAGGATCTCAAGAGATCCCTTTGATCTCTTTTCTACGGGGTCTGACCGCTCAGT  
5256 AAACCTCAGCTTAAGGGATTTGGTCAATGAGATTAACAAGAGATCTTCAACCTTA  
4327 AAACCTCAGCTTAAGGGATTTGGTCAATGAGATTAACAAGAGATCTTCAACCTTA  
5316 TTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGG  
4387 TTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGG  
5376 CAGTACCAATGCTTAATCAGTGAAGGACCTATCTCAGCGATCTGTCTATTTTCGG  
4447 CAGTACCAATGCTTAATCAGTGAAGGACCTATCTCAGCGATCTGTCTATTTTCGG  
5436 CATAGTTGCTGATCTCCCGTGTGTGATATACTACGATACGGGAGGGCTTACCC  
4507 CATAGTTGCTGATCTCCCGTGTGTGATATACTACGATACGGGAGGGCTTACCC  
5496 CCCAGTGTGCAATGATACCGCGAGACCCAGCTCACCGGCTCCAGATTTATC  
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5556 AAACCAAGCGGAGGCGAGAGAGCGAGAGAGTGTCTGCAACTTTTATCCGCG  
4627 AAACCAAGCGGAGGCGAGAGAGCGAGAGTGTCTGCAACTTTTATCCGCG  
5616 CCAAGTCTTAATTTGTTGCCGAGAGCTAGATTAAGTTAGTTCCCAAGTTAAATAG  
4687 CCAAGTCTTAATTTGTTGCCGAGAGCTAGATTAAGTTAGTTCCCAAGTTAAATAG  
5676 CAAAGTTGTTGCCATTTGCTACAGGCACTGTGTGTGTCAACGCTCGTCTGTTGGTAT  
4747 CAAAGTTGTTGCCATTTGCTACAGGCACTGTGTGTGTCAACGCTCGTCTGTTGGTAT  
5736 ATTCAAGTCTCGGTTCCCAAGCATCAAGGCGAGTTACATGATCCCCCATGTTGTG  
4807 ATTCAAGTCTCGGTTCCCAAGCATCAAGGCGAGTTACATGATCCCCCATGTTGTG  
5796 AGCGGTTAGCTCTCTCGGTCTCCGATCGTTGTGCAGAACTAGTTGGCGCGCAGT  
4867 AGCGGTTAGCTCTCTCGGTCTCCGATCGTTGTGCAGAACTAGTTGGCGCGCAGT  
5856 ACTCATGTTATAGCGAGCATGCTAATAATCTCTTACTGTCAATGCCATCCGTAAG  
4927 ACTCATGTTATAGCGAGCATGCTAATAATCTCTTACTGTCAATGCCATCCGTAAG  
5916 TTCTGTGACTGTGTGAGTACTCAACCAAGTCAATCTCAGAACTAGTTATGCGGCG  
4987 TTCTGTGACTGTGTGAGTACTCAACCAAGTCAATCTCAGAACTAGTTATGCGGCG  
5976 TTGCTCTCTGCGCGCGTCAATACGGGATTAATACGGCGCCACATAGCAGAACTTTT  
5047 TTGCTCTCTGCGCGCGTCAATACGGGATTAATACGGCGCCACATAGCAGAACTTTT  
6036 GCTCATCATATGGAAGAGTTCTTTCGGGGCGAAATCTCTCAAGGATCTTACCGCT  
5107 GCTCATCATATGGAAGAGTTCTTTCGGGGCGAAATCTCTCAAGGATCTTACCGCT  
6096 ATCCAGTTTCGATGTAAACCCACTCGTCGACCCAACTGATCTTCAGCATCTTTTAC  
5167 ATCCAGTTTCGATGTAAACCCACTCGTCGACCCAACTGATCTTCAGCATCTTTTAC  
6156 CACGGTTTCGGGTGAGCAAAAACAGGAGGCAAAATGCGGCAAAAAGGGAAT  
5227 CACGGTTTCGGGTGAGCAAAAACAGGAGGCAAAATGCGGCAAAAAGGGAAT  
6216 GACACGGAATGTTGAATCTCATCTCTCTCTTTTCAATATATTTGAAGCAT  
5287 GACACGGAATGTTGAATCTCATCTCTCTCTTTTCAATATATTTGAAGCAT  
6276 GGGTTATGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATTAACCT  
5347 GGGTTATGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATTAACCT

633 GGTTCGCGCACATTCCCGAAAGTGCCACCTGACGTC 6375  
 640 GGTTCGCGCACATTCCCGAAAGTGCCACCTGACGTC 6416

961 standard; DNA; 5446 BP.

EB 002 (first entry)

lla luciferase vector pcDNA3.

lla luciferase; sea pansy; cell proliferation disorder;  
 ne isorder; hypogammaglobulinemia; haematologic condition; anaemia;  
 las; cancer; human immunodeficiency virus; HIV;  
 ue; white cell infiltrative disorder; organ failure;  
 rop ic condition; gonadal failure; bone disorder; muscle disorder;  
 opo sis; endocrine condition; vascular disorder; atherogenesis;  
 A3; 1s.

bet 1.

018 314-A2.

CV- 101.

PR- 101; 2001WO-US013512.

PR- 100; 2000US-00559874.

JN- 100; 2000US-00586339.

W-} CHEMICON INT.

J;

20 1-041420/05.

monitoring cell proliferation for monitoring treatment of a subject,  
 ris a obtaining light emission data from cell containing Renilla  
 fer se for specific time, and detecting a change in the data.

Fig 1A-B; 52pp; English.

invitation describes a novel method for measuring proliferation of a  
 or population of cells. The method comprises obtaining light  
 ion data from a cell containing a Renilla luciferase over a period  
 ime cell proliferation of a cell or a population of cells can be  
 are by a change in light emission data indicating proliferation. A  
 or containing the Renilla luciferase enzyme is useful for diagnosing  
 ll proliferative disorder including: neoplasia or cancer, viral  
 ides or disease e.g. Human immunodeficiency virus (HIV), immune  
 adies e.g. hypogammaglobulinemia and haematologic conditions e.g.  
 nian tissue white cell infiltrative disorders, organ failure,  
 rop ic conditions, gonadal failure, conditions of bone and muscle  
 esoporosis, endocrine conditions and vascular disorders e.g.  
 rogenesis, by transfecting a cell obtained from a subject with the  
 or id comparing the light emission data from the cell to that of a  
 wh does not have a cell proliferative disorder. A difference in  
 light emission is indicative of a cell proliferative disorder. The vector  
 is useful for determining the effect of an agent on cell  
 efection, by transfecting a cell obtained from a sample with the  
 or, and contacting the transfected cell with an agent suspected of  
 ating cell proliferation under conditions that allow the agent and  
 el to interact, and comparing the light emission data from the cell  
 ne light emission data from the cell in the absence of the agent. The  
 ds are useful for drug discovery and drug screening, and in  
 oring the treatment of a subject diagnosed with a cell proliferative  
 order. This sequence is the vector pcDNA3 into which Renilla  
 ferase (AAS1816) is placed before transformation of cells with the

CC vector to allow measurement of cell proliferation described in the method  
 CC of the invention  
 XX Sequence 5446 BP; 1255 A; 1417 C; 1390 G; 1384 T; 0 U; 0 Other  
 SQ  
 Query Match 56.1%; Score 3578.4; DB 6; Length 5446  
 Best Local Similarity 88.9%; Pred. No. 0;  
 Matches 4141; Conservative 0; Mismatches 16; Indels 503; Gap 8;  
 QY 1750 GAGCTCCAGCTTTTCTGAGCGCGAAAGAACAGCTGGGGGTATCTAGGGGGTATCT  
 DB 1256 GGGCTCTATGGCTTCTGAGCGCGAAAGAACAGCTGGGGGTATCTAGGGGGTATCT  
 QY 1810 GCCCTGTAGCGCGCATTAAGCGCGCGGTGGTGTACCGCGAGCGTGAC  
 DB 1316 GCCCTGTAGCGCGCATTAAGCGCGCGGTGGTGTACCGCGAGCGTGAC  
 QY 1870 ACTTGCAGCGCGCTAGCGCGCGCTCTTTCGCTTTCTTCCCTTCTCTCTCG  
 DB 1376 ACTTGCAGCGCGCTAGCGCGCGCTCTTTCGCTTTCTTCCCTTCTCTCTCG  
 QY 1930 CGCGCGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTTCGGAT  
 DB 1436 CGCGCGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTTCGGAT  
 QY 1989 TTTACGGCACCTCGACCCCAAAAACCTTGATTAGGGTGTGTTACGCTAGTGC  
 DB 1496 TTTACGGCACCTCGACCCCAAAAACCTTGATTAGGGTGTGTTACGCTAGTGC  
 QY 2049 GCCTGTATAGACGGTTTTCGCGCTTTGAGCTTGGAGTCCACGTTCTTTAATAC  
 DB 1556 GCCTGTATAGACGGTTTTCGCGCTTTGAGCTTGGAGTCCACGTTCTTTAATAC  
 QY 2109 CTGTGTTCCAAACTGGACACACTCAACCTATCTCGGTCTATCTTTGATTT  
 DB 1616 CTGTGTTCCAAACTGGACACACTCAACCTATCTCGGTCTATCTTTGATTT  
 QY 2169 GATTTTCGCGATTTTCGCGCTATTTGGTTAAAAATAGCTGATTAAACAAAAT  
 DB 1676 GATTTTCGCGATTTTCGCGCTATTTGGTTAAAAATAGCTGATTAAACAAAAT  
 QY 2229 GAATTAATTTCTGTGGAATCCCGGGAGCTTGATATATCCATTTTCGGATCTGAT  
 DB 1736 GAATTAATTTCTGTGGAATCCCGGGAGCTTGATATATCCATTTTCGGATCTGAT  
 QY 2289 GAGCGGAAAGAACACAGCTGTGGATGTGTGTCAGTTAGGGTGTGAAAGTCCC  
 DB 1745 GAGCGGAAAGAACACAGCTGTGGATGTGTGTCAGTTAGGGTGTGAAAGTCCC  
 QY 2349 CCCCCA-GCAGGAGAGATGCAAGCATGTCATCTCAATTAGTCAGCAACCCAGG  
 DB 1788 CCCCCAAGGAGAGATGCAAGCATGTCATCTCAATTAGTCAGCAACCCAGG  
 QY 2408 AAGTCCAGGCTTCCCGAGCGAGATATGCAAGCATGTCATCTCAATTAG  
 DB 1848 AAGTCCAGGCTTCCCGAGCGAGATATGCAAGCATGTCATCTCAATTAG  
 QY 2468 ACCATAGTCCCGCTTCACTCCGCGCATCCCGCGCTTCACTCCGCGCATCC  
 DB 1908 ACCATAGTCCCGCTTCACTCCGCGCATCCCGCGCTTCACTCCGCGCATCC  
 QY 2528 TCTCGCGCGCTGCTGACTAATTTTTTTTATTTATGAGAGCGCGAGCGCGCC  
 DB 1968 TCTCGCGCGCTGCTGACTAATTTTTTTTATTTATGAGAGCGCGAGCGCGCC  
 QY 2588 TCTGAGCTATTCCAGAGTAGTAGGAGGCTTTTTTTGGAGGCTTAGGCTTTTGC  
 DB 2028 TCTGAGCTATTCCAGAGTAGTAGGAGGCTTTTTTTGGAGGCTTAGGCTTTTGC  
 QY 2648 C-----GATCAAGAGACAGGATGAGGA  
 DB 2088 CTCCCGGGAGCTTGATATATCCATTTTCGGATCTGATCAAGAGAGGATGAGGA





D:	390	(AGTTCCGTTGATGTCGTTCCGCTCCAAAGCTGGGCTGTGTGCAGAAACCCCGGTTTCAGCC	396
Q:	489	(GACCGCTCGCCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTAAAGACACGACTTT	4955
D:	395	(GACCGCTCGCCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTAAAGACACGACTTT	4026
Q:	495	ATCGGCACTGGCAGGAGCACTGGTAAACAGGATTTAGCAGACGAGGTATGTAGCGGTGC	5015
D:	402	ATCGGCACTGGCAGGAGCACTGGTAAACAGGATTTAGCAGACGAGGTATGTAGCGGTGC	4086
Q:	501	TACAGAGTTCTTTGAAGTGGTGGCCCTAACTACGGCTACACTAGAGAACAGTATTTGGTAT	5075
D:	408	TACAGAGTTCTTTGAAGTGGTGGCCCTAACTACGGCTACACTAGAGAACAGTATTTGGTAT	4146
Q:	509	(TCGGCTCTGCTGAAGCCAGTTACTCTCGAAAAAGAGTTGGTAGCTCTTTGATCCGGCAA	5135
D:	414	CTGGCTCTGCTGAAGCCAGTTACTCTCGAAAAAGAGTTGGTAGCTCTTTGATCCGGCAA	4206
Q:	513	AAAAACACCGCTGGTATAGCGGTGGTTTTTTTGGTTTGAAGCAGCAGATTACGGCAGAAA	5195
D:	420	AAAAACACCGCTGGTATAGCGGTGGTTTTTTTGGTTTGAAGCAGCAGATTACGGCAGAAA	4266
Q:	519	AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGA	5255
D:	426	AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGA	4326
Q:	525	AACTCACGTTTAAAGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACTAGATCCCT	5315
D:	432	AACTCACGTTTAAAGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACTAGATCCCT	4386
Q:	531	TTTAAATTAANAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACCTTGGTCTGA	5375
D:	438	TTTAAATTAANAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACCTTGGTCTGA	4446
Q:	537	CAGTTACCAATGCTTAATCAGTGAAGGACCTATCTCAGCGCATCTGCTATTTTCGTTCAATC	5435
D:	444	CAGTTACCAATGCTTAATCAGTGAAGGACCTATCTCAGCGCATCTGCTATTTTCGTTCAATC	4506
Q:	543	CATAGTTGCCCTGACTCCCGCTCGTGTAGATAAACTACGATACGGAGGGCTTACCATCTGG	5495
D:	450	CATAGTTGCCCTGACTCCCGCTCGTGTAGATAAACTACGATACGGAGGGCTTACCATCTGG	4566
Q:	549	CCGAGTGTGCAATGATACCGGAGACCCACGCTCAACCGGCTCCAGATTATTCAGCAAT	5555
D:	456	CCGAGTGTGCAATGATACCGGAGACCCACGCTCAACCGGCTCCAGATTATTCAGCAAT	4626
Q:	555	AAACCGCAGCCGGAAGGCGGAGCGCAGAGTGGTCTGCAACTTATTCGCGCTCCAT	5615
D:	462	AAACCGCAGCCGGAAGGCGGAGCGCAGAGTGGTCTGCAACTTATTCGCGCTCCAT	4686
Q:	561	CCAGTCTTAATAATTGTTGCCGGGAAGCTAGAGTAAAGTAGTTCGCCAGTTAATAGTTTGG	5675
D:	468	CCAGTCTTAATAATTGTTGCCGGGAAGCTAGAGTAAAGTAGTTCGCCAGTTAATAGTTTGG	4746
Q:	567	CACGTTGTTGCCATTTGCTAAGGCAATCGTGGTGTCAACGCTCGTTCGTTTGGTATGCTTTC	5735
D:	474	CACGTTGTTGCCATTTGCTAAGGCAATCGTGGTGTCAACGCTCGTTCGTTTGGTATGCTTTC	4806
Q:	573	ATTCAGCTCCGGTTCCCAAGATCMAGGCCAGTTACATGATCCCGCATGTTGTGCAAAAA	5795
D:	480	ATTCAGCTCCGGTTCCCAAGATCMAGGCCAGTTACATGATCCCGCATGTTGTGCAAAAA	4866
Q:	579	AGCGTTAGCTCCTTCCGCTCCTCCGATCGTTGTGAGAAAGTGGCCGCGAGTGTATC	5855
D:	486	AGCGTTAGCTCCTTCCGCTCCTCCGATCGTTGTGAGAAAGTGGCCGCGAGTGTATC	4926
Q:	585	ACTCATGGTTATGGCAGCATGTCATTAATCTCTTACTGTATGCCATCCGTAAGATGCTTT	5915
D:	492	ACTCATGGTTATGGCAGCATGTCATTAATCTCTTACTGTATGCCATCCGTAAGATGCTTT	4986
Q:	591	TTCTGTGACTGTGTGAGTACTCAACCAAGTCAATCTTGAGAAATAGTGTATCGCGGCAACGAG	5975
D:	498	TTCTGTGACTGTGTGAGTACTCAACCAAGTCAATCTTGAGAAATAGTGTATCGCGGCAACGAG	5046

the control of the CMV promoter, creating plasmid pHsp60. In order to explore the potential of a DNA-based therapy of insulin-labile diabetes mellitus (IDDM), the effect of immunisation of NOD spontaneously developing IDDM, with pHsp60 was examined. A pcDNA3 plasmid was as effective at inhibiting the development of diabetes as was the pHsp60 plasmid. Despite the absence of any induced specific effects on the autoimmunity to Hsp60, the NOD diabetogenic process: down-regulation of T-cell antigen presentation and the induction of IgG2b antibodies to Hsp60 and its cognate p277. A CpG oligonucleotide (see ABLG3541), present in the CpG island of the human Hsp60 gene, reproduced the effects of pcDNA3 on the development of diabetes. The invention therefore provides a method for the treatment or prevention of autoimmune diseases by administering a DNA vaccine which includes a CpG motif and which encodes a protein associated with autoimmune diseases, especially the protein Hsp60.

[illegible]

Q: TCGTTTCCGGAGCGCGGCTGGATGATCTCCAGCGCGGGATCTCATGCTGGAGTTCT 3635  
D: ----- 2997  
Q: TCGCCCACTAGGGGAGGCTAACTGAACAACGAGGAGACATAACCGAAGAACCC 3695  
D: ----- 2997  
Q: GCGATGACGGCAATAAAAGACAGATAAAAACGACGGTGTGGGTGTTTGTTCATAA 3755  
D: ----- 2997  
Q: ACGGGGTTTCGCTCCAGGGCTGGCACTCTGTGCGATACCCACCGAGACCCCATTTGGGG 3815  
D: ----- 2997  
Q: CAAATAGCGCGGCTTCTTCTTTTCCCAACCCACCCCAAGTTTCGGGTGAGGCCCC 3875  
D: ----- 2997  
Q: ACGCTCGAGCCAAAGTCGGGGCGGCGAGCCCTGCGCATAGCCTCAGTGTACGAGATTT 3935  
D: -----ACGAGATTT 3006  
Q: CAAATCCACCGCGCTTCTATGAAGTTTGGGCTTCGGAATCGTTTTCGGGACGCGCG 3995  
D: CAAATCCACCGCGCTTCTATGAAGTTTGGGCTTCGGAATCGTTTTCGGGACGCGCG 3066  
Q: CCGATGATCCTCCAGCGCGGATCTCATGCTGGAGTTCTTCGCCCAACCCCACTTTGTT 4055  
D: CGATGATCTCCAGCGCGGATCTCATGCTGGAGTTCTTCGCCCAACCCCACTTTGTT 3126  
Q: TAATGAGCTTAATAGTTTACAAATAAGCAATAGCATCAAAATTTTCAAAATAAGC 4115  
D: TAATGAGCTTAATAGTTTACAAATAAGCAATAGCATCAAAATTTTCAAAATAAGC 3186  
Q: AATTTTTCACGCAATCTAGTTGTGGTTTGTCTCAAACTCATCAATGATCTTATCATGT 4175  
D: AATTTTTCACGCAATCTAGTTGTGGTTTGTCTCAAACTCATCAATGATCTTATCATGT 3246  
Q: CTGTATACCGCTCAGCTAGAGCTTGGGTAAATCATGTCTATAGCTTGTCTTCTGT 4235  
D: CTGTATACCGCTCAGCTAGAGCTTGGGTAAATCATGTCTATAGCTTGTCTTCTGT 3306  
Q: GTGAATTTGTATCCGCTCAAAATTCACAACAATACGAGCGGAAGCATAAAGTTAA 4295  
D: GTGAATTTGTATCCGCTCAAAATTCACAACAATACGAGCGGAAGCATAAAGTTAA 3366  
Q: AGCTCGGGTGCCCTAATGAGTGAAGCTAACTCAATTAATGGCTTGGCTCAGTCCCGC 4355  
D: AGCTCGGGTGCCCTAATGAGTGAAGCTAACTCAATTAATGGCTTGGCTCAGTCCCGC 3426  
Q: TTCCAGTCGGGAAACCTGTCTGCCAGCTGCAATTAATGAATCGGCAACCGCGGGAG 4415  
D: TTCCAGTCGGGAAACCTGTCTGCCAGCTGCAATTAATGAATCGGCAACCGCGGGAG 3486  
Q: AGCGGTTTTCGATTTGGGCGCTTTCGCTTCTCGCTCACTGACTCGCTCGCTCGGT 4475  
D: AGCGGTTTTCGATTTGGGCGCTTTCGCTTCTCGCTCACTGACTCGCTCGCTCGGT 3546  
Q: CTTTCGCTCGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAAATAGCTTATCCACAGA 4535  
D: CTTTCGCTCGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAAATAGCTTATCCACAGA 3606  
Q: ATCAGGGGATAACGCAAGGAAGCAATGTGAGCAAAAGGCGAGCAAAAGCCAGGAACCG 4595  
D: ATCAGGGGATAACGCAAGGAAGCAATGTGAGCAAAAGGCGAGCAAAAGCCAGGAACCG 3666  
Q: TAAAAAGCGCGCTTCTCGCTTTCATAGGCTCCGCGCCCTGACGAGCATCACAA 4655  
D: TAAAAAGCGCGCTTCTCGCTTTCATAGGCTCCGCGCCCTGACGAGCATCACAA 3726

QY 4656 AAATCGACGCTCAAGTCAGAGTGGGAAACCCGACAGGACTATAAAGATAACCT 4735  
Db 3727 AAATCGACGCTCAAGTCAGAGTGGGAAACCCGACAGGACTATAAAGATAACCT 3786  
QY 4716 TCCGCTCGGAGCTCCCTCGTGGCTCTCTCTGTTCGACCCCTGCGGCTTACCG 4775  
Db 3787 TCCGCTCGGAGCTCCCTCGTGGCTCTCTCTGTTCGACCCCTGCGGCTTACCG 3846  
QY 4776 GTCCGCTTCTCCCTTCGGGAGCGTGGCGCTTCTCATAGCTCAGCTGTAC 4835  
Db 3847 GTCCGCTTCTCCCTTCGGGAGCGTGGCGCTTCTCATAGCTCAGCTGTAC 3906  
QY 4836 CAGTTCGGTGTAGGTCTGTCTCCAAAGCTGGGCTGTGTGACGAAACCCCGG 4895  
Db 3907 CAGTTCGGTGTAGGTCTGTCTCCAAAGCTGGGCTGTGTGACGAAACCCCGG 3966  
QY 4896 CGACCGCTGGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCCCGTAAAGC 4955  
Db 3967 CGACCGCTGGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCCCGTAAAGC 4026  
QY 4956 ATCCCACTGGCAGCAGCCACTCGTAAACAGATTAGCAGAGCGAGGTATGTAC 5015  
Db 4027 ATCCCACTGGCAGCAGCCACTCGTAAACAGATTAGCAGAGCGAGGTATGTAC 4086  
QY 5016 TACAGAGTCTTGAAGTGGTGGCTTAACCTACCGCTACACTAGAGAACACAGTAT 5075  
Db 4087 TACAGAGTCTTGAAGTGGTGGCTTAACCTACCGCTACACTAGAGAACACAGTAT 4146  
QY 5076 CTGCGCTCTGTGAAGCCAGTTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATC 5135  
Db 4147 CTGCGCTCTGTGAAGCCAGTTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATC 4206  
QY 5136 ACAAACACCGCTGTAGCGGTGTTTTTTTGTTCAGAGCAGCAGATTACGCG 5195  
Db 4207 ACAAACACCGCTGTAGCGGTGTTTTTTTGTTCAGAGCAGCAGATTACGCG 4266  
QY 5196 AAAGATCTCAAGAAAGATCTTTTGTCTACCGGCTCTGACGCTCAGTC 5255  
Db 4267 AAAGATCTCAAGAAAGATCTTTTGTCTACCGGCTCTGACGCTCAGTC 4326  
QY 5256 AAATCAAGTAAAGGATTTTGTCTAGAGATTATCAAAAGAGTCTTACCTT 5315  
Db 4327 AAATCAAGTAAAGGATTTTGTCTAGAGATTATCAAAAGAGTCTTACCTT 4386  
QY 5316 TTTAAATTTAAATGAAGTTTTAAATCAATCTAAAGTATATATAGTAAACTTC 5375  
Db 4387 TTTAAATTTAAATGAAGTTTTAAATCAATCTAAAGTATATATAGTAAACTTC 4446  
QY 5376 CAGTTACCAATGCTTAAATCAGTGAGGACCTATCTCAGCGATCTGTCTATTTC 5435  
Db 4447 CAGTTACCAATGCTTAAATCAGTGAGGACCTATCTCAGCGATCTGTCTATTTC 4506  
QY 5436 CATAGTTGCTCACTCCCGCTGTGTAGATACTAGATAACCGAGGGGCTTACC 5495  
Db 4507 CATAGTTGCTCACTCCCGCTGTGTAGATACTAGATAACCGAGGGGCTTACC 4566  
QY 5496 CCCAGTGTCTCAATGATACCGCGAGACCCAGCTCACCGCTCCAGATTATC 5555  
Db 4567 CCCAGTGTCTCAATGATACCGCGAGACCCAGCTCACCGCTCCAGATTATC 4626  
QY 5556 AAAACGAGCGCGGAGAGGGCGAGCGAGAGTGTCTCTGCAACTTTATCCGC 5615  
Db 4627 AAAACGAGCGCGGAGAGGGCGAGCGAGAGTGTCTCTGCAACTTTATCCGC 4686  
QY 5616 CCAGTCTATTATTTGTTCGGGAGAGCTAGAGTAAGTAGTTCGCCAGTTAAATAG 5674  
Db 4687 CCAGTCTATTATTTGTTCGGGAGAGCTAGAGTAAGTAGTTCGCCAGTTAAATAG 4746  
QY 5676 CAAAGTTGTTCGCAATTTGTACAGGATCGTGTGTACCGCTCGCTGTTTGGTAT 5735  
Db 4747 CAAAGTTGTTCGCAATTTGTACAGGATCGTGTGTACCGCTCGCTGTTTGGTAT 4804  
QY 5736 ATTACGCTCCGGTTCCTCAACGATCAAGCGAGGTTATCATGATCCCCCATGTTGTG 5795

|||||TCAGCTCCGGTCCCAACGATCAGCGGAGTTACATGATCCCCCATTTGTGCAAAA 4866  
 |||||CGGTTAGCTCTTCGGTCTCCGATCGTTGTGTCAGAAAGTTGGCCGCGAGTTATC 5855  
 |||||CGGTTAGCTCTTCGGTCTCCGATCGTTGTGTCAGAAAGTTGGCCGCGAGTTATC 4926  
 |||||TCATGGTTATGCGAGCACTGCATATTCCTTACTGTGTCATGCCATCCGTAAGATGCTT 5915  
 |||||TCATGGTTATGCGAGCACTGCATATTCCTTACTGTGTCATGCCATCCGTAAGATGCTT 4986  
 |||||CTGTGACTGCTGAGTACTCAACCAAGTCACTCTGAGAATAGTGTATGCGCGACCGAG 5975  
 |||||CTGTGACTGCTGAGTACTCAACCAAGTCACTCTGAGAATAGTGTATGCGCGACCGAG 5046  
 |||||GCTCTTGCCCGCGCTCAATACCGGATAATACCGCGCCACATAGCAGAACTTTAAAGT 6035  
 |||||GCTCTTGCCCGCGCTCAATACCGGATAATACCGCGCCACATAGCAGAACTTTAAAGT 5106  
 |||||TCATCAATTCGAAAAGCTTCTCGGGCGGAAACTCTCAAGGATCTTACCGCTGTGAG 6095  
 |||||TCATCAATTCGAAAAGCTTCTCGGGCGGAAACTCTCAAGGATCTTACCGCTGTGAG 5166  
 |||||CCAGTTTCGATGTAAACCACTCTGTGCAACCAACTGATCTTTCAGCATCTTTTACTTTTAC 6155  
 |||||CCAGTTTCGATGTAAACCACTCTGTGCAACCAACTGATCTTTCAGCATCTTTTACTTTTAC 5226  
 |||||GGCTTCTGGGTAGCAAAAACAGGAAGCAAAATCCCGCAAAAAGGGAATAAGGCG 6215  
 |||||GGCTTCTGGGTAGCAAAAACAGGAAGCAAAATCCCGCAAAAAGGGAATAAGGCG 5286  
 |||||CAGGAAATGTTGAATCACTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 6275  
 |||||CAGGAAATGTTGAATCACTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5346  
 |||||GTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAACAAATAGG 6335  
 |||||GTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAACAAATAGG 5406  
 |||||TTCCGGCGACATTTCCCGGAAAAGTCCACCTGACGTC 6375  
 |||||TTCCGGCGACATTTCCCGGAAAAGTCCACCTGACGTC 5446

andard; DNA; 6082 BP.

(first entry)

1-XG1-051 PSMA antibody light chain DNA.

tate specific membrane antigen; carcinoma; sarcoma; cancer;  
 oma; therapy; N-acetylated alpha-linked acidic dipeptidase;  
 olase; dipeptidyl dipeptidase IV; gamma-glutamyl hydrolase;  
 antibody; ds.

s.

3-A2.

; 2002WO-US033944.

; 2001US-0335215P.

; 2002US-0362747P.

; 2002US-0412618P.

IA DEV CO LLC.

PI Maddon RJ, Donovan GP, Olson WC, Schuelke N, Gardner J, Ma  
 XX WPI; 2003-403281/38.

XX Novel isolated antibody which binds to epitope on prostate spec  
 PT membrane antigen, and competitively inhibits binding of second  
 PT to its target epitope on the antigen, useful for treating prost  
 PT cancer.

XX Claim 1; Page 213-216; 238pp; English.

XX The invention relates to an antibody or its antigen-binding fra  
 CC which specifically binds to epitope on prostate specific membra  
 CC (PSMA), and competitively inhibits the specific binding of a se  
 CC antibody to its target epitope on PSMA. The invention is useful  
 CC diagnosing, treating or preventing PSMA-mediated disease such a  
 CC cancer or non-prostate cancer bladder chosen from cancer includ  
 CC transitional cell carcinoma, pancreatic cancer including pancre  
 CC carcinoma, lung cancer including non-small cell lung carcinoma,  
 CC cancer including conventional renal cell carcinoma, sarcoma inc  
 CC soft tissue sarcoma, breast cancer including breast carcinoma,  
 CC cancer including glioblastoma multiforme, neuroendocrine carcin  
 CC cancer including colonic carcinoma, testicular cancer including  
 CC testicular embryonal carcinoma, or melanoma including malignant  
 CC The invention is useful also for inhibiting or enhancing folate  
 CC activity of a folate hydrolase polypeptide, N-acetylated alpa-  
 CC acidic dipeptidase (NALADase) polypeptide, activity of a NALADase polypept  
 CC dipeptidyl dipeptidase IV activity of a dipeptidyl dipeptidase  
 CC polypeptide, gamma-glutamyl hydrolase activity of a gamma-gluta  
 CC hydrolase polypeptide. The present sequence is human PSMA antib  
 CC chain DNA

XX Sequence 6082 BP; 1418 A; 1594 C; 1551 G; 1519 T; 0 U; 0 Other;  
 SQ Query Match 56.1%; Score 3578.4; DB 7; Length 6082;  
 Best Local Similarity 88.9%; Pred. No. 0;  
 Matches 1414; Conservative 0; Mismatches 16; Indels 503;

QY 1750 GAGCTCCAGCTTTTCTGAGCGGGAAGAACAGCCAGCTGGGGCTCTAGGGGGTATCC  
 DB 1892 GGGCTCTATGGCTTCTGAGCGGGAAGAACAGCCAGCTGGGGCTCTAGGGGGTATCC  
 QY 1810 GCCCTGTAGCGCGCATTTAAGCGCGCGGGGTGTGGTTACGCGCAGCGTGAC  
 DB 1952 GCCCTGTAGCGCGCATTTAAGCGCGCGGGGTGTGGTTACGCGCAGCGTGAC  
 QY 1870 ACTTGCAGCGCCCTAGCGCGCGCTCTTTCGCTTCTTCCCTTCTTCTTCGC  
 DB 2012 ACTTGCAGCGCCCTAGCGCGCGCTCTTTCGCTTCTTCCCTTCTTCTTCGC  
 QY 1930 CGCGGGCTTCCCGTCAAGCTCTAATTCGGGGC-TCCTTTAGGGTTCCGANT  
 DB 2072 CGCGGGCTTCCCGTCAAGCTCTAATTCGGGGCANTCCCTTAGGGTTCCGANT  
 QY 1989 TTTACGCACTCGACCCCAAAAACTTGTATTAGGGTGAAGTTCACGTAAGTG  
 DB 2132 TTTACGCACTCGACCCCAAAAACTTGTATTAGGGTGAAGTTCACGTAAGTG  
 QY 2049 GCCCTGTAGCGCGTTTTCGCGCTTGTGACCGTGGAGTCCACGTTCTTTATAG  
 DB 2192 GCCCTGTAGCGCGTTTTCGCGCTTGTGACCGTGGAGTCCACGTTCTTTATAG  
 QY 2109 CTGTTCAAAACTGGAACAACACACTCAACCTTATCTCGGTCTATTCTTTTGAATTT  
 DB 2252 CTGTTCAAAACTGGAACAACACACTCAACCTTATCTCGGTCTATTCTTTTGAATTT  
 QY 2169 GATTTTGGGATTTTGGCTATTGGTTAAATAAATGAGCTGATTTAAACAAAAATTT  
 DB 2312 GATTTTGGGATTTTGGCTATTGGTTAAATAAATGAGCTGATTTAAACAAAAATTT  
 QY 2229 GAATTTAATTTCTGTGAATGCGCGGAGCTTGTATATCCATTTTTCGATCTGATC  
 DB 2372 GAATTTAATTT

Q: 228 GAGCGGAAGAACCACTGTGGATGTGTCTAGTTAGGTGTGGAAGTCCCGAGCT 2348  
D: 228 -----CTGTGGAAATGTGTCTAGTTAGGTGTGGAAGTCCCGAGCT 2423  
Q: 234 CCCCAGCAGAGATGCAAGCATGATCTCAATAGTCAGCAACAGGTGTGA 2407  
D: 242 CCCCAGCAGCAGAGATGCAAGCATGATCTCAATAGTCAGCAACAGGTGTGA 2483  
Q: 240 AGTCCCAAGCTCCCGAGCAGAGATGCAAGCATGATCTCAATAGTCAGCA 2467  
D: 248 AGTCCCAAGCTCCCGAGCAGAGATGCAAGCATGATCTCAATAGTCAGCA 2543  
Q: 246 ACCATAGTCCCGCCCTAACTCCGCCATCCGCCCTTAAGTCGCCAGTTCGCCCAT 2527  
D: 254 ACCATAGTCCCGCCCTAACTCCGCCATCCGCCCTTAAGTCGCCAGTTCGCCCAT 2603  
Q: 252 TCTCCGCCCATGGCTGACTAAATTTTATTTATGTCAGAGCCGAGCGCTCCGCC 2587  
D: 260 TCTCCGCCCATGGCTGACTAAATTTTATTTATGTCAGAGCCGAGCGCTCCGCC 2663  
Q: 258 TCTGAGCTATTCAGAGATGAGGAGGCTTTTGGAGCCCTAGGCTTTTGCAAGAT 2647  
D: 266 TCTGAGCTATTCAGAGATGAGGAGGCTTTTGGAGCCCTAGGCTTTTGCAAAAG 2723  
Q: 264 -----GATCAAGAGACAGATGAGATCGTTT 2675  
D: 272 TCTCCGGGAGCTGTATATCCATTTTCGGATCTGATCAAGAGACAGGATGAGATCGTTT 2783  
Q: 267 CGCATGATTGAACAAGATGATTGCACGACAGGTCTCCGCCGCTTGGGTGGAGAGCTA 2735  
D: 278 CGCATGATTGAACAAGATGATTGCACGACAGGTCTCCGCCGCTTGGGTGGAGAGCTA 2843  
Q: 273 TTGGGCTATGACTGGGCAACAAGCAATCGGTGCTCTGATCCGCGCTGTTCCGCTG 2795  
D: 284 TTGGGCTATGACTGGGCAACAAGCAATCGGTGCTCTGATCCGCGCTGTTCCGCTG 2903  
Q: 279 TCAAGCGAGGGCGCGGCTCTCTTTTGTCAAGCAGACCTGTCGGTGCCCTGAATGAA 2855  
D: 290 TCAAGCGAGGGCGCGGCTCTCTTTTGTCAAGCAGACCTGTCGGTGCCCTGAATGAA 2963  
Q: 285 CTGCAAGAAGAGCAGCGCGCTATCGTGCTGGCCACAGCGGCTTCTCTCGCAGCT 2915  
D: 296 CTGCAAGAAGAGCAGCGCGCTATCGTGCTGGCCACAGCGGCTTCTCTCGCAGCT 3023  
Q: 292 GTGCTCGAGTTGTCTAGAGCGGGAAGGACTGCTGCTATTGGGCGAAGTCCCGGG 2975  
D: 302 GTGCTCGAGTTGTCTAGAGCGGGAAGGACTGCTGCTATTGGGCGAAGTCCCGGG 3083  
Q: 297 CAGGATCTCTGTCACTCAGCTTGAATCGGGTACCTCGCCCAATTCGACCACCAAGCAACAT 3035  
D: 308 CAGGATCTCTGTCACTCAGCTTGAATCGGGTACCTCGCCGAGAAAGATCCCATCATGGCTGATGCA 3143  
Q: 303 AAGCGCGGTGATACGCTTGAATCGGGTACCTCGCCCAATTCGACCACCAAGCAACAT 3095  
D: 314 AAGCGCGGTGATACGCTTGAATCGGGTACCTCGCCCAATTCGACCACCAAGCAACAT 3203  
Q: 309 CAGATCGAGGAGCAGCTACTCGGATGGAAGCGGCTTGTGATCAGGATGATCTGGAC 3155  
D: 320 CAGATCGAGGAGCAGCTACTCGGATGGAAGCGGCTTGTGATCAGGATGATCTGGAC 3263  
Q: 315 GAGAGCATCAGGGGCTCCGCCAGCGGACTGTTCCGAGGCTCAAGCGGAGCATGCC 3215  
D: 326 GAGAGCATCAGGGGCTCCGCCAGCGGACTGTTCCGAGGCTCAAGCGGAGCATGCC 3323  
Q: 321 GAGCGGAGAGATCTCGTCTGTGACCCATGCGCATGCTGCTTGGCCGAATATCATGTGGAA 3275  
D: 328 GAGCGGAGAGATCTCGTCTGTGACCCATGCGCATGCTGCTTGGCCGAATATCATGTGGAA 3383  
Q: 327 AATGGCGCGTTTCTGGATTCATCGACTGTGCGCGCTGGGTGTGGCGGACCGCTATCAG 3335  
D: 328 AATGGCGCGTTTCTGGATTCATCGACTGTGCGCGCTGGGTGTGGCGGACCGCTATCAG 3443

Q: 3336 GACATAGCTTGGCTACCCGCTGATTTCTGAAGAGCTTGGCGCGAATGGGC 3395  
D: 3444 GACATAGCTTGGCTACCCGCTGATTTCTGAAGAGCTTGGCGCGAATGGGC 3503  
Q: 3396 TTCTCTGTGCTTTACGGTATCGCGCTCCCGATTCGAGCGCATCGCTTCTA 3455  
D: 3504 TTCTCTGTGCTTTACGGTATCGCGCTCCCGATTCGAGCGCATCGCTTCTA 3563  
Q: 3456 CTTGACGAGTTCTTCGAGCGGACTCTGGGTTTGGAAATGACGACCAAGCG 3515  
D: 3564 CTTGACGAGTTCTTCGAGCGGACTCTGGGTTTGGAAATGACGACCAAGCG 3623  
Q: 3516 ACTGCCATCAGGAGATTTCCGATTTCCACCGCGCTTCTATGAAGGTTGGGC 3575  
D: 3624 ACTGCCATC----- 3633  
Q: 3576 TCGTTTTCGGGAGCGCGGCTGGATGATCTCCAGCGCGGGATCTCATGCTG 3635  
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Q: 3636 TCGCCACCCCTAGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAA 3695  
D: 3634 ----- 3633  
Q: 3696 GCGCATGACGGCAATAAAAGACAGAAATAAACGCGGCTGTGGGTCTGTTG 3715  
D: 3634 ----- 3633  
Q: 3756 ACGGGGGTTGCTCCCGAGGCTGGCAGCTCTGTGATACCCACCGAGACCCCT 3815  
D: 3634 ----- 3633  
Q: 3816 CCAATACGCGCGGTTTCTTCTTTTCCACCCACCCCAAGTTTCGGGTG 3875  
D: 3634 ----- 3633  
Q: 3876 AGGGCTCGAGCCAAAGCTCGGGCGGAGCCCTGCATAGCTCAGTCTAC 3935  
D: 3634 -----ACGAGTTT 3642  
Q: 3936 CGATTCCAGCGCGCTTCTATGAAGGTTGGCTTCGGAATCGTTTTCGGG 3995  
D: 3643 CGATTCCAGCGCGCTTCTATGAAGGTTGGCTTCGGAATCGTTTTCGGG 3762  
Q: 3996 CTGGATGATCTCCAGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCA 4055  
D: 3703 CTGGATGATCTCCAGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCA 3762  
Q: 4056 TATTGAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTTCA 4115  
D: 3763 TATTGAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTTCA 3822  
Q: 4116 ATTTTTCACCTGCATTTCTAGTTGGTTTGTTCGCAACTCATCATGATCTTA 4175  
D: 3823 ATTTTTCACCTGCATTTCTAGTTGGTTTGTTCGCAACTCATCATGATCTTA 3880  
Q: 4176 CTGTATACCGTCCGCTCTAGCTAGAGCTTGGCTTAATCATGTCTATGCTGT 4235  
D: 3883 CTGTATACCGTCCGCTCTAGCTAGAGCTTGGCTTAATCATGTCTATGCTGT 3942  
Q: 4236 GTGAAATTTGTTATCGGCTCAAAATTCACACAACATACGAGCGGAGCATAAA 4295  
D: 3943 GTGAAATTTGTTATCGGCTCAAAATTCACACAACATACGAGCGGAGCATAAA 4002  
Q: 4296 AGCCTTGGGTGCTTAATGAGTGAGCTTAATCATTAATTTGGTTGGCTCACT 4355  
D: 4003 AGCCTTGGGTGCTTAATGAGTGAGCTTAATCATTAATTTGGTTGGCTCACT 4062  
Q: 4356 TTTCCAGTCCGGAACCTGTGCTGCGAGCTGATTAATGAATCGGCCAACGGC 4415  
D: 4063 TTTCCAGTCCGGAACCTGTGCTGCGAGCTGATTAATGAATCGGCCAACGGC 4122  
Q: 4416 AGCGGCTTGGGTATTGGGCGCTCTTCCGCTTCTCTGCTCACTGACTCGCTCG 4475

|||||  
3CGGTTTTCGGTATTTGGGCGCTTCTCCGCTTCTCGCTCACTGACTCGCTCGCTCGGT 4182

TTCCGCTCGCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATTCACAGA 4535

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CAGGGGATAACGCGAGGAAGAAATGTGAGCGAAAGGCGCAGCAAAAGGCGCAGGAACGG 4595

CAGGGGATAACGCGAGGAAGAAATGTGAGCGAAAGGCGCAGCAAAAGGCGCAGGAACGG 4302

AAAAGGCGCGGTGCTGGCGTTTTCATAGAGCTCCGCCCTGACGAGCATCACAA 4655

AAAAGGCGCGGTGCTGGCGTTTTCATAGAGCTCCGCCCTGACGAGCATCACAA 4362

ATCGACGCTCAAGTCAGAGGTGGCAAAACCCGACAGGACTATATAAGATACCAAGCGGTT 4715

ATCGACGCTCAAGTCAGAGGTGGCAAAACCCGACAGGACTATATAAGATACCAAGCGGTT 4422

CCCTCGAAGCTCCCTCGTGGCTCTCTGTTTCGACCTGCGCGCTTACCGGATACCT 4775

CCCTCGAAGCTCCCTCGTGGCTCTCTGTTTCGACCTGCGCGCTTACCGGATACCT 4482

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CCGCTTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGTAGGTATCT 4542

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GTTCCGTTAGGTGTTTCCGCTCGAAGCTGGGCTGTGACGAAACCCCGCTTCAGCC 4602

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ACCGTCGCGCTTATTCGGTAACTATCGTCTTGAGTCCAAACCGGTAAAGCACGACTT 4662

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ACTCAGTTAAAGGATTTGGTCAAGATATCAAAAGGATCTTCACTAGATCCCT 5022

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TAGTTTGCCTGACTCCCGTGGTGTAGTAACTACTACGATACGGAGGGCTTACCATCTGG 5202

CCAGTGTCTGCAATGATACCGCGAGACCCAGCTCACCGGCTCCAGATTTATCAGCAAT 5555

5203	CCCCAGTGTCTGCAATGATACCGCGAGACCCACGCTCACGGCTCCAGATTATAT	Db
5556	AAACCAAGCCAGCCGGAAGGCGAGCGCAAGAGTGTCTCTGCAACTTTATATCCGC	Qy
5563	AAACCAAGCCAGCCGGAAGGCGAGCGCAAGAGTGTCTCTGCAACTTTATATCCGC	Db
5616	CCAGTCTATTAATTTGTTCGCGGAAGCTAGAGTAAGTACGTTCGCCAGTTAAATAG	Qy
5323	CCAGTCTATTAATTTGTTCGCGGAAGCTAGAGTAAGTACGTTCGCCAGTTAAATAG	Db
5676	CAACGTTGTTGCCAATTTGCTACAGGCAATCGTGTGTGTCAAGCTCGTGTGTTGATAT	Qy
5383	CAACGTTGTTGCCAATTTGCTACAGGCAATCGTGTGTGTCAAGCTCGTGTGTTGATAT	Db
5736	ATTTCAGCTCCGGTTCCCAAGGATCAAGGGGAGTTACATGATCCCCCATGTTGTG	Qy
5443	ATTTCAGCTCCGGTTCCCAAGGATCAAGGGGAGTTACATGATCCCCCATGTTGTG	Db
5796	AGCGTTTAGCTCTCTTGGTCTCTCCGATCGTTGTTCAGAACTAAGTTGGCCGCACT	Qy
5503	AGCGTTTAGCTCTCTTGGTCTCTCCGATCGTTGTTCAGAACTAAGTTGGCCGCACT	Db
5856	ACTCATGTTTATGCGCAGCACTGCATTAATTTCTTTACTGTCAATGCCATCCGTAAAG	Qy
5563	ACTCATGTTTATGCGCAGCACTGCATTAATTTCTTTACTGTCAATGCCATCCGTAAAG	Db
5916	TTCTGTGACTCGGTGAGTACTCAACCAAGTCAATTTCTGAGAAATAGTGTATCGGGG	Qy
5623	TTCTGTGACTCGGTGAGTACTCAACCAAGTCAATTTCTGAGAAATAGTGTATCGGGG	Db
5976	TTGCTCTTGGCCGCGCTCAATACGGGATTAATCCGGCGCCACATAGCAGAACTTTT	Qy
5683	TTGCTCTTGGCCGCGCTCAATACGGGATTAATCCGGCGCCACATAGCAGAACTTTT	Db
6036	GCTCATCATTTGGAAAAAGTTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCT	Qy
5743	GCTCATCATTTGGAAAAAGTTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCT	Db
6096	ATCCAGTTTCGAGTGTAAACCACTCGTCGACCACTGATCTTCAGCACTCTTTTAC	Qy
5803	ATCCAGTTTCGAGTGTAAACCACTCGTCGACCACTGATCTTCAGCACTCTTTTAC	Db
6156	CAGCGTTTCTCGGGTGAGCAAAAAAGGAAGGCAAAATGCCGCAAAAAAGGGAAT	Qy
5863	CAGCGTTTCTCGGGTGAGCAAAAAAGGAAGGCAAAATGCCGCAAAAAAGGGAAT	Db
6216	GACACGGAAATGTTGAATATCTACATCTCTTCTTTTCAATATATTTTGAAGCAT	Qy
5923	GACACGGAAATGTTGAATATCTACATCTCTTCTTTTCAATATATTTTGAAGCAT	Db
6276	GGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACA	Qy
5983	GGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACA	Db
6336	GGTTCGCGCACATTTTCCCGGAAAGTGCCACTGAGCTC 6375	Qy
6043	GGTTCGCGCACATTTTCCCGGAAAGTGCCACTGAGCTC 6082	Db

RESULT 13	
AAAD56211	
ID	AAAD56211 standard; DNA; 6082 BP.
XX	
XX	
AC	AAAD56211;
XX	
DT	07-AUG-2003 (first entry)
XX	
DE	Human AB-PG1-XG1-026 PSMA antibody light chain DNA.
XX	
KW	Human; Prostate specific membrane antigen; carcinoma; sarcoma;
KW	PSMA; melanoma; therapy; N-acetylated alpha-linked acidic dipep-
KW	folate hydrolase; dipeptidyl dipeptidase IV; gamma-glutamyl hyc-
KW	NAALADase; antibody; ds.





[illegible]

3983	CTGTATACCGTGCACCTCTAGCTAGAGCTTGGCGTAATCATGGTCACTAGCTGTG	Db
4236	GTGAATTTGTTATTCGCTCACAATTTCCACAACAATACAGACCGGAAGCATAA	Qy
3943	GTGAATTTGTTATTCGCTCACAATTTCCACAACAATACAGACCGGAAGCATAA	Db
4296	AGCTGGGTGCTTAATGATGAGCTTAACTCACTAATTAATTTGGTTGCGCTCACT	Qy
4003	AGCTGGGTGCTTAATGATGAGCTTAACTCACTAATTAATTTGGTTGCGCTCACT	Db
4356	TTTCCAGTCCGGGAAAACCTGTGTCGCCAGCTGCATTAATGAATCGGCCAACGGCG	Qy
4063	TTTCCAGTCCGGGAAAACCTGTGTCGCCAGCTGCATTAATGAATCGGCCAACGGCG	Db
4416	AGCGGTTTCGGTATTTGGGGCGCTCTTCGCTTCCTCGCTCATCTGACTCGCTGGG	Qy
4123	AGCGGTTTCGGTATTTGGGGCGCTCTTCGCTTCCTCGCTCATCTGACTCGCTGGG	Db
4476	CGTTTCGGCTCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATC	Qy
4183	CGTTTCGGCTCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGGTTATC	Db
4536	ATCAGGGGATTAACGACGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCGCAG	Qy
4243	ATCAGGGGATTAACGACGAAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCGCAG	Db
4596	TAAAGAGGCGCGTTCTCGTGGCGTTTTTCCATAGGCTCCGCCCGCTGACGAGCA	Qy
4303	TAAAGAGGCGCGTTCTCGTGGCGTTTTTCCATAGGCTCCGCCCGCTGACGAGCA	Db
4656	AAATCGACGCTCAAGTCAGAGGTGGCGAAACCGACAGGACTATAAAGATACCA	Qy
4363	AAATCGACGCTCAAGTCAGAGGTGGCGAAACCGACAGGACTATAAAGATACCA	Db
4716	TCCCGCTGGAAGCTCCCTCGTGGGCTCTCCGTGTTCCGACCCCTGCGCTTACCGG	Qy
4423	TCCCGCTGGAAGCTCCCTCGTGGGCTCTCTCTGTTCCGACCCCTGCGCTTACCGG	Db
4776	GTCCGCTCTTCTCCCTTCCGGGAAAGCGTGGCGCTTTCTCATAGCTCAACGCTGTAG	Qy
4483	GTCCGCTCTTCTCCCTTCCGGGAAAGCGTGGCGCTTTCTCATAGCTCAACGCTGTAG	Db
4836	CAGTTCCGGTGTAGTCTGCTCCAGCTGCGGCTGTGTGCAACCCCGCTTACCGG	Qy
4543	CAGTTCCGGTGTAGTCTGCTCCAGCTGCGGCTGTGTGCAACCCCGCTTACCGG	Db
4896	CGACGCTGCGCCTTATCCGGTAACTATCGCTTGTAGTCCAAACCCCGCTTACGAC	Qy
4603	CGACGCTGCGCCTTATCCGGTAACTATCGCTTGTAGTCCAAACCCCGCTTACGAC	Db
4956	ATCGCCACTGCGACAGCCCATGCTAAACAGATTAACAGAGCGAGGTATGTAGG	Qy
4663	ATCGCCACTGCGACAGCCCATGCTAAACAGATTAACAGAGCGAGGTATGTAGG	Db
5016	TACAGATTTCTTGAAGTGTGGCTTAACCTACGCTACACTAGAAGAACAGTAT	Qy
4723	TACAGATTTCTTGAAGTGTGGCTTAACCTACGCTACACTAGAAGAACAGTAT	Db
5076	CTGGCTCTGCTGAAGCGAGTTACTCTTTCGGAAAAGAGTTGGTAGCTCTTGATG	Qy
4783	CTGGCTCTGCTGAAGCGAGTTACTCTTTCGGAAAAGAGTTGGTAGCTCTTGATG	Db
5136	ACAAACCAACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTAACGCC	Qy
4843	ACAAACCAACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTAACGCC	Db
5196	AAAAGGATCTCAAGAGATCCCTTTTGAATCTTTTCTTACGGGGTCTGACGCTCACTG	Qy
4903	AAAAGGATCTCAAGAGATCCCTTTTGAATCTTTTCTTACGGGGTCTGACGCTCACTG	Db
5256	AAACTCAGTTAAGGGAATTTTGGTCATGAGTATCAAAAGGATCTTCACTT	Qy
4963	AAACTCAGTTAAGGGAATTTTGGTCATGAGTATCAAAAGGATCTTCACTT	Db



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|||||CGGCTTTCCCGTCAAGCTCTAAATCGGGGCG-TCGCTTTTAGGGTTCCGATTTAGTGC 1988  
|||||CGGCTTTCCCGCTCAAGCTCTAAATCGGGGCGATCCCTTTAGGGTTCCGATTTAGTGC 2131  
|||||TACGCGACCTCGACCCCAAAAACTTGAATTAGGGTGATGGTTCAAGTAGTGCGCCATC 2048  
|||||TACGCGACCTCGACCCCAAAAACTTGAATTAGGGTGATGGTTCAAGTAGTGCGCCATC 2191  
|||||CCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTTAATAGTGGACT 2108  
|||||CCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTTAATAGTGGACT 2251  
|||||TGTTCCAAACTGGAAACAACACTCAACCCTATCTCGGTCTATTCTTTTGAATTTATAAGG 2168  
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|||||ATTAATTT----- 2380  
|||||GGCGGAAGAAACGAGCTGTGGAATGTGTCTCAGTTAGGGTGTGGAAGTCCCGAGGT 2348  
|||||-----CTGTGGAAATGTGTCTCAGTTAGGGTGTGGAAGTCCCGAGGT 2423  
|||||CCA- GCAGGCAGAAATATGCAAGCATGCTCTCAATTAGTCAAGCAACAGGTGTGGA 2407  
|||||CCAGGCAGGCAGAAATATGCAAGCATGCTCTCAATTAGTCAAGCAACAGGTGTGGA 2483  
|||||GTCCCGAGCTCCCGAGCGGAGAGATGCAAAAGCATGCTCTCAATTAGTCAAGCA 2467  
|||||GTCCCGAGCTCCCGAGCGGAGAGATGCAAAAGCATGCTCTCAATTAGTCAAGCA 2543  
|||||CATAGTCCCGCCCTAATCCCGCCATCCCGCCCTAATCCCGCCAGTTCGCGCCAT 2527  
|||||CATAGTCCCGCCCTAATCCCGCCATCCCGCCCTAATCCCGCCAGTTCGCGCCAT 2603  
|||||TCCGCCCCATGGCTGACTAATTTTTTTTATTTATGAGAGCGCGAGGCCCTCGGCC 2587  
|||||TCCGCCCCATGGCTGACTAATTTTTTTTATTTATGAGAGCGCGAGGCCCTCGGCC 2663  
|||||TGAGCTATTCCAGAGTAGGAGGCTTTTTTGGAGGCTTAGGCTTTTGGCAAGAT 2647  
|||||TGAGCTATTCCAGAGTAGGAGGCTTTTTTGGAGGCTTAGGCTTTTGGCAAAAG 2723  
|||||-----GATCAAGAGACAGGATGAGGATCGTTT 2675  
|||||CCCGGAGCTTGATATATCCATTTTCGGATCTGATCAAGAGACAGGATGAGGATCGTTT 2783  
|||||CATGATTGAACAAGATGAGATTGCAAGAGTTCTCCGGCGCTTTGGGTGAGAGGCTA 2735  
|||||CATGATTGAACAAGATGAGATTGCAAGAGTTCTCCGGCGCTTTGGGTGAGAGGCTA 2843  
|||||CGGCTATGACTGGGCAACAAGCAATCGGCTCTGATGCGCGCTGTTCCGGCTG 2795  
|||||CGGCTATGACTGGGCAACAAGCAATCGGCTCTGATGCGCGCTGTTCCGGCTG 2903  
|||||AGCGAGGGGCGCCCGGCTCTTTTGTCAAGACCGGCTGTCCGGTGCCTGAATGAA 2855  
|||||AGCGAGGGGCGCCCGGCTCTTTTGTCAAGACCGGCTGTCCGGTGCCTGAATGAA 2963  
|||||GCAAGGACGAGGCGAGCGGCTGATCGTGGCTGGGCAAGACGAGGCGGCTTCTGGCGAGCT 2915  
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Db 2964 CTCGAGGACGAGGCGAGCGGCTATCTGTGGCTGGCCACGACGCGGCGGCTTCTTTCG  
Qy 2916 GTGCTCGACGTTGTCTCATGAAGCGGGAAGGGAATGGGCTGTCTATTGGGCGGAAGTG  
Db 3024 GTGCTCGACGTTGTCTCATGAAGCGGGAAGGGAATGGGCTGTCTATTGGGCGGAAGTG  
Qy 2976 CAGGATCTCTCTGTCATCTCACCTTGTCTTGGCTGGCGGAGAAAGTATCCATCATGGCT  
Db 3084 CAGGATCTCTCTGTCATCTCACCTTGTCTTGGCTGGCGGAGAAAGTATCCATCATGGCT  
Qy 3036 ATGCGGCGGCTGCTACATCGCTTGTATCCGGCTACCTGGCCCATTTGCAACCAAGCG  
Db 3144 ATGCGGCGGCTGCTACATCGCTTGTATCCGGCTACCTGGCCCATTTGCAACCAAGCG  
Qy 3096 CGCATCGAGCGAGCACGCTACTCGGATCGGAAGCGGCTTGTGCGATCAGGATGAT  
Db 3204 CGCATCGAGCGAGCACGCTACTCGGATCGGAAGCGGCTTGTGCGATCAGGATGAT  
Qy 3156 GAGAGCATCAGGGGCTCGGCGCAGCCGAACTGTTCCGACAGGCTCAAGGGCGAGC  
Db 3264 GAGAGCATCAGGGGCTCGGCGCAGCCGAACTGTTCCGACAGGCTCAAGGGCGAGC  
Qy 3216 GACGGCAGGATCTCGTGTGACCCATGCGGAGGCTGCTTTCGGAATATCATG  
Db 3324 GACGGCAGGATCTCGTGTGACCCATGCGGATGCGGATGCTTTCGGAATATCATG  
Qy 3276 AATGGCGCTTTCTCGGATTCATCGACTGTGGCGGCTGCTGCTGGGCGGAGCGC  
Db 3384 AATGGCGCTTTCTCGGATTCATCGACTGTGGCGGCTGCTGCTGGGCGGAGCGC  
Qy 3336 GACATAGCGTTGGCTACCGGTGATATTGCTGAAGAGCTTGGCGGCGAAATGGGCT  
Db 3444 GACATAGCGTTGGCTACCGGTGATATTGCTGAAGAGCTTGGCGGCGAAATGGGCT  
Qy 3396 TTCTCTGTGCTTACGGTATCGCGCTTCCGATTCGAGCGCATCGCCTTCTAT  
Db 3504 TTCTCTGTGCTTACGGTATCGCGCTTCCGATTCGAGCGCATCGCCTTCTAT  
Qy 3456 CTTGACAGGTTCTTCTGAGCGGAGCTCTGGGGTTGGAATGACCGACCGAGCGA  
Db 3564 CTTGACAGGTTCTTCTGAGCGGAGCTCTGGGGTTGGAATGACCGACCGAGCGA  
Qy 3516 ACCTGCGCATCAGGATTTGATTTCCACCGCGGCTTCTATGAAAGGTTGGGCT  
Db 3624 ACCTGCGCATC-----  
Qy 3576 TCGTTTTCCGGGACGCGCGCTGGATGATCTCTCCAGCGCGGGGATCTCATGCTGG  
Db 3634 -----  
Qy 3636 TCGCCCACTAGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAG  
Db 3634 -----  
Qy 3696 GCGCATGACGCAATAAAGACAGAAATAAAGCAAGCAAGTGTGGGTGTTGT  
Db 3634 -----  
Qy 3756 ACGCGGGGTTCCGTTCCAGGGCTGGCACTCTGTGATACCCCAACGAGACCCCA  
Db 3634 -----  
Qy 3816 CCAATACGCGCGGCTTTCTTCTTTTCCACCCCGCCCGCAAGTTCCGGGTGA  
Db 3634 -----  
Qy 3876 AGGGCTCGACCAACGTTCCGGGCGGCGAGGCGCTGCGCATAGCTCAGTGTCTACG  
Db 3634 -----ACC  
Qy 3936 CGATTCCACCGCGCTTCTATGAAGGTTGCGGCTTTCGGAATCGTTTTCCGGGT  
Db 3643 CGATTCCACCGCGCTTCTATGAAGGTTGCGGCTTTCGGAATCGTTTTCCGGGT

Q: CTGATGATCCTCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCCACCCCACTTGT 4055  
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D: TATTGACAGCTTATAAAGTTACAAATAAGCAATAGCATCACAAATTTCAAAATAAGC 3822  
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D: AATTTTTTCACTGCAATCTAGTTGTGGTTTGTCCAAACTCATCAATGATCTTATCATGT 3882  
Q: CTGTATACCGTCACTCTAGCTAGAGCTTGGGGTAATCATGTGTCATGCTGTTTCCTGT 4235  
D: CTGTATACCGTCACTCTAGCTAGAGCTTGGGGTAATCATGTGTCATGCTGTTTCCTGT 3942  
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D: GTCAAAATTTGTTATCCGCTCAAAATCCACAAACATACGAGCGGAGCATAAAGTGTA 4002  
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Q: AAGCGGTTTGGCTAATTTGGGGCTCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 4475  
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Q: GTCCGCTTTCTCCCTTCCGGAAGCGTGGCGCTTCTCATAGCTCAGCTGAGGTATCT 4835  
D: GTCCGCTTTCTCCCTTCCGGAAGCGTGGCGCTTCTCATAGCTCAGCTGAGGTATCT 4542  
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D: CATTCGCTGATAGTCTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 4602  
Q: CACCGCTGGCCCTTATCCGCTTACATGCTCTGAGTCCGCTTCCGCTTCCGCTTCCGCT 4955  
D: CACCGCTGGCCCTTATCCGCTTACATGCTCTGAGTCCGCTTCCGCTTCCGCTTCCGCT 4662  
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Q: CTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTTTGAT 5076  
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Q: ACTCATGTTATGCGGAGCTCATGATTAATCTTCTTACTGTATGCTGATCGTAA 5563  
D: ACTCATGTTATGCGGAGCTCATGATTAATCTTCTTACTGTATGCTGATCGTAA 5622  
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D: TTCTGTGACTGTGAGTACTCAACAGTCAATCTGAGTAATAGTGTATCGGCG 5682  
Q: TTGCTCTTCCCGCGGTCAATACGGGTAATACCGGCCACATAGCAGAACTTT 5976  
D: TTGCTCTTCCCGCGGTCAATACGGGTAATACCGGCCACATAGCAGAACTTT 6035  
Q: GCTCATCTTGAAGAACGTTCTTCGCGGGGAGAACTCTCAAGGATCTTACCGCT 6036  
D: GCTCATCTTGAAGAACGTTCTTCGCGGGGAGAACTCTCAAGGATCTTACCGCT 5742  
Q: GCTCATCTTGAAGAACGTTCTTCGCGGGGAGAACTCTCAAGGATCTTACCGCT 5743  
D: GCTCATCTTGAAGAACGTTCTTCGCGGGGAGAACTCTCAAGGATCTTACCGCT 5802  
Q: ATCCAGTTCGATGTAACCCACTCGTGCAACCACTGATCTTCCAGGATCTTTTAC 6096  
D: ATCCAGTTCGATGTAACCCACTCGTGCAACCACTGATCTTCCAGGATCTTTTAC 6155  
Q: ATCCAGTTCGATGTAACCCACTCGTGCAACCACTGATCTTCCAGGATCTTTTAC 5803  
D: ATCCAGTTCGATGTAACCCACTCGTGCAACCACTGATCTTCCAGGATCTTTTAC 5862  
Q: CAGCGCTTCTGCGGTGAGCAAAACAGGAGGCAAAATGCCGCAAAAGGGAAT 6156  
D: CAGCGCTTCTGCGGTGAGCAAAACAGGAGGCAAAATGCCGCAAAAGGGAAT 6215

3CGTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCGCAAAAAGGGAATAAGGCG 5922

CACGGAATGTTGGAATCATCATACTCTCTCTTTTCAATATTATTGAAGCATTATATCA 6275

CACGGAATGTTGGAATCATCATACTCTCTCTTTTCAATATTATTGAAGCATTATATCA 5982

GTTATTGTCTCATGAGCGGAATACATATTTGAAATGTTATTAGAAAAATTAACAATAGG 6335

GTTATTGTCTCATGAGCGGATACATATTTGAAATGTTATTAGAAAAATTAACAATAGG 6042

TTCCGGCGACATTTCCCGAAAAGTGCCACCTGACGTC 6375

TTCCGGCGACATTTCCCGAAAAGTGCCACCTGACGTC 6082

andard: DNA: 6085 BP.

(first entry)

1-XG1-069 PSMA antibody light chain DNA.

tate specific membrane antigen; carcinoma; sarcoma; cancer; oma; therapy; N-acetylated alpha-linked acidic dipeptidase; olase; dipeptidyl dipeptidase IV; gamma-glutamyl hydrolase; antibody; ds.

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3-A2.

• : 2002WO-US033944.

; 2001US-0335215P.  
; 2002US-0362747P.  
; 2002US-0412618P.

A DEV CO LLC.

Donovan GP, Olson WC, Schuelke N, Gardner J, Ma D;

03281/38.

ted antibody which binds to epitope on prostate specific antigen, and competitively inhibits binding of second antibody et epitope on the antigen, useful for treating prostate

ae 216-219: 238pp: English.

on relates to an antibody or its antigen-binding fragment specifically binds to epitope on prostate specific membrane antigen competitively inhibits the specific binding of a second , its target epitope on PSMA. The invention is useful for treating or preventing PSMA-mediated disease such as prostate on-prostate cancer bladder chosen from cancer including l cell carcinoma, pancreatic cancer including pancreatic duct lung cancer including non-small cell lung carcinoma, kidney using conventional renal cell carcinoma, sarcoma including sarcoma, breast cancer including breast carcinoma, brain using glioblastoma multiforme, neuroendocrine carcinoma, colon using colonic carcinoma, testicular cancer including embryonic carcinoma, or melanoma including malignant melanoma. on is useful also for inhibiting or enhancing folate hydrolase a folate hydrolase polypeptide, N-acetylated alpha-linked ipitadase (NALADase) activity of a NALADase polypeptide, dipeptidase IV activity of a dipeptidyl dipeptidase IV

CC polypeptide, gamma-glutamyl hydrolase activity of a gamma-gluta  
CC hydrolase polypeptide. The present sequence is human PSMA antib  
CC chain DNA

Query Match 56.1%; Score 3578.4; DB 7; Length 6085;  
 Best Local Similarity 88.9%; Pred. No. 0;  
 Matches 4141; Conservative 0; Mismatches 16; Indels 503;  
 Sequence 6085 BP; 1412 A; 1601 C; 1556 G; 1516 T; 0 U; 0 Other;

QY 1750 GAGCTCCAGCTTTTCTGAGCGCGAAAGAACCAAGCTGGGGCTCTAGGGGATATCC  
| | | | |  
Db 1895 GGGCTCTATGGCTTCTGAGCGCGAAAGAACCAAGCTGGGGCTCTAGGGGATATCC

Qy 1810 GCCCTGTAGCGCGGCATTAAAGCGCGGGGTGTGGTGGTTACGCCGACGGTGAC  
Db 1955 GCCCTGTAGCGCGGCATTAAAGCGCGGGGTGTGGTGGTTACGCCGACGGTGAC

Qy 1870 ACTTGCAGCGCCTAGCGCGCTCTTTTCGCTTTCTTCCCTTCTTCTCGC  
Db 2015 ACTTGCAGCGCCTAGCGCGCTCTTTCGCTTTCTTCCCTTCTTCTCGC

Qy		CGCCGGCTTTCCCCGTCAGACTCTAAATCGGGGC-TCCCTTTAGGGTTCGGATT
Db		CGCCGGCTTTCCCCGTCAGACTCTAAATCGGGGCATCCCCTTTAGGGTTCGGATT

[illegible]

Qy	2049	2195
	GCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAAATAG	GCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAAATAG

Qy	2109	CTTGTTC	CAAACTG	GGAACA	CACACT	CAACCT	TATCT	CGGTCT	ATTC	TTTTG	ATTT
D <sub>b</sub>	2255	CTTGTTC <th>CAAACTG</th> <th>GGAACA</th> <th>CACACT</th> <th>CAACCT</th> <th>TATCT</th> <th>CGGTCT</th> <th>ATTC</th> <th>TTTTG</th> <th>ATTT</th>	CAAACTG	GGAACA	CACACT	CAACCT	TATCT	CGGTCT	ATTC	TTTTG	ATTT

**Qy** 2169 GATTTTGCCGATTTCGGCCTATTGGTTAAAAAATCGAGCTGATTTAACAAAATT  
|||||  
**Dd** 2315 GATTTTGGGGAATTTCGGCCTATTGGTTAAAAAATCGAGCTGATTTAACAAAATT

QY	2229	GAATTAATCTCTGGAATGCGCGGAGCTTGATATCAATTTTCGGATCTGATC
Db	2375	GAATTAATT-----GAATTAATT-----

**Qy** 2289 GAGCGGAAAGAACCAGCTGTGGAAATGTGTGTCACTTAGGTCGTGGAAAGTCCC  
| | | | | | | | | | | | | | | | | | | | | |  
**Dd** 2384 -----CTGTGGAAATGTGTGTCACTTAGGTCGTGGAAAGTCCC

Qy 2349 CCCCA-GCAGGCGAAGTATGCAAGCATCTCAATTAGTCAGCAACGAGG  
|||  
Db 2427 CCCGAGCGCGAAGTATGCAAGCATCTCAATTAGTCAGCAACGAGG

QY	2408	2487
	AAGTCCCAGGCTCCCAGCAGGCAGAGTATGCAAGCATGTCATCTCAATTAG	AAGTCCCAGGCTCCCAGCAGGCAGAGTATGCAAGCATGTCATCTCAATTAG

Qy 2468 ACCATAGTCCCGCCCTAACTACCTCGGCCATCCGCGCCCTAACTCGGCCAGTTCC  
|||  
Db 2547 ACCATAGTCCCGCCCTAACTCGGCCATCCGCGCCCTAACTCGGCCAGTTCC

Qy	2528	TCTCGCCCCATGGCTGACTAA	TTTTTTTTTTATTTATG	CAGAGCGCGCGCC
Db	2607	TCTCGCCCCATGGCTGACTAA	TTTTTTTTTTATTTATG	CAGAGCGCGCGCC

Qy	2588	TCTGAGCTATTCCAGAAGT	AGT	AGG	AGG	CTTTTTTT	GGAGG	CTTAGG	CTTTTTC
Db <th>2667</th> <th>TCTGAGCTATTCCAGAAGT</th> <th>AGT</th> <th>AGG</th> <th>AGG</th> <th>CTTTTTTT</th> <th>GGAGG</th> <th>CTTAGG</th> <th>CTTTTTC</th>	2667	TCTGAGCTATTCCAGAAGT	AGT	AGG	AGG	CTTTTTTT	GGAGG	CTTAGG	CTTTTTC

Qy	2648	C	-----GATCAAGAGACAGGATGAGG
Db	2727	CTCCCCGGAGCTTGTATATCCATTTTCGGATCTGATCAAGAGACAGGATGAGG	

267 CCGATGATTGAA CAAAGATGGATTGCA CGCAGGTTCTCCGCCGCTTGCGTGGAGAGCTA 2735  
278 CCGATGATTGAA CAAAGATGGATTGCA CGCAGGTTCTCCGCCGCTTGCGTGGAGAGCTA 2846  
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284 TCCGGCTATGACTGGGCACACAGCAATCGGCTGCTGATGCGCGCGGTTCGCGCTG 2906  
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314 ATGGCGGCGCTGCATACGCTTGATCCGGCTACTCTGCCCATTCGACCAACGAGGAAACAT 3206  
309 CGCATCCAGCGAGCAGCATCTCGATGGAAGCGGCTCTTCGATCAGGATGATCTGGAC 3155  
320 CGCATCCAGCGAGCAGCATCTCGATGGAAGCGGCTCTTCGATCAGGATGATCTGGAC 3266  
315 GAAGAGATCAGGGGCTCGCGCAGCGGAACTGTTGCGCAGGCTCAAGCGGAGCATGCC 3215  
326 GAAGAGATCAGGGGCTCGCGCAGCGGAACTGTTGCGCAGGCTCAAGCGGAGCATGCC 3326  
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333 GACATAGCGTTGGCTACCCGTGATAATGCTGAAGAGCTTGGCGGCGAAATGGGCTGACCGC 3395  
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Db 5626 TTCTGTGACTGGTGGTACTCAACCAAGTCAATCTGAGAAATAGTGTATGCGGCG  
Qy 5976 TTGCTCTTGGCCGGCGTCAATACCGGATAATACCGGCGCCACATAGCAGAACTTT  
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Qy 6036 GCTCATCATTTGGAAAAAGTTTCTTCGGGGCGGAAAACTCTCAAGGATCTTTACCGCT  
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Search completed: July 15, 2004, 08:09:01  
Job time : 2340 secs





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QY 3005 TGCCGAGAAAGTATCCATCATATGGCTGAATGCAATGGCGGGCTGCATACGCTTGA  
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 CCTGAGTC 6375  
 CTTGAGTC 5653

plication US/08646538  
 7881

# NATION:

Pavliakis, George N.  
 Gaitanaris, George A.  
 Stauber, Roland H.  
 Vournakis, John N.

VENTION: Mutant Aequorea victoria Fluorescent

VENTION: Proteins Having Increased Cellular Fluorescence

SEQUENCES: 37

NCE ADDRESS:

: Townsend and Townsend and Crew LLP  
 Two Embarcadero Center, 8th Floor

n Francisco

alifornia

USA

11-3834

ADABLE FORM:

PE: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

Patent in Release #1.0, Version #1.30

LICATION DATA:

ON NUMBER: US/08/646,538

TE: No. 6027881 yet assigned

ATION: 435

ENT INFORMATION:

ber, Kenneth A.

ION NUMBER: 31,677

/DOCKET NUMBER: 015280-249000

CATION INFORMATION:

: (415) 576-0200

(415) 576-0300

OR SEQ ID NO: 5:

ABACTERISTICS:

6238 base pairs

cleic acid

ISS: single

linear

PE: DNA

1..6238

FORMATION: /note= "pFRED7"

Query Match 56.1%; Score 3578.4; DB 3; Length 6238;  
 Best Local Similarity 88.9%; Pred. No. 0;  
 Matches 4141; Conservative 0; Mismatches 16; Indels 503;

Qy 1750 GAGCTCCAGCTTTTCTGAGCGGAAAGAACCCAGCTGGGGCTCTAGGGGGTATCC  
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D1	342		GAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGCGGACATGCC		3479
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Db	4639	GTCCGCTTTTCTCCCTTCGGGAAGCGTGGCGCTTTTCTCATAGCTCACGCTGTAG	4698
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Qy	6216	GACACGGAAATGTTGAATACTCATACTCTCTCTTTTCAATATATTTCAGCAT
Db	6079	GACACGGAAATGTTGAATACTCATACTCTCTCTTTTCAATATATTTCAGCAT
Qy	6276	GGGTATTGTCTCATGACGGGATACATATTTGAAATGTTATTTAGAAAAATAACA
Db	6139	GGGTATTGTCTCATGACGGGATACATATTTGAAATGTTATTTAGAAAAATAACA
Qy	6336	GGTTCGGCGGCACATTTCCCGGAAAAAGTGCCACTGACGTC 6375
Db	6199	GGTTCGGCGGCACATTTCCCGGAAAAAGTGCCACTGACGTC 6238

RESULT 3

US-09-503-222-5

; Sequence 5, Application US/09503222

; Patent No. 6265548

; GENERAL INFORMATION:

; APPLICANT: Pavlakis, George N.

; APPLICANT: Gaitanaris, George A.

; APPLICANT: Stauber, Roland H.

; APPLICANT: Vournakis, John N.

; TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent

; TITLE OF INVENTION: Proteins Having Increased Cellular Fluores

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patencin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/503,222

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/646,538

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Kenneth A.

; REGISTRATION NUMBER: 31,677

; REFERENCE/DOCKET NUMBER: 015280-249000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6238 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; FEATURE:

; NAME/KEY: -

; LOCATION: 1..6238

HER INFORMATION: /note= "pPRED7"		
Q1	56.1%; Score 3578.4; DB 3; Length 6238;	
B1	cal Similarity 88.9%; Pred. No. 0;	
M1	cal Conservative 0; Mismatches 16; Indels 503; Gaps 5;	
Q1	175 GAGCTCAGCTTTTCTCAGGCGGAAAGAACAGCTGGGGCTTAGGGGGTATCCCCACGC 1809	
D1	204 GGGCTCTATGGCTTCTCAGGCGGAAAGAACAGCTGGGGCTTAGGGGGTATCCCCACGC 2107	
Q1	181 GCGCTGTAGCGGCGCATTAAGCGCGCGGGTGCTGTACGCGCAGCGGTGACCGGTAC 1869	
D1	210 GCGCTGTAGCGGCGCATTAAGCGCGCGGGTGCTGTACGCGCAGCGGTGACCGGTAC 2167	
Q1	187 ACTTGCCAGCGCGCTAGCGCGCGCTCTCTTTGCTTTCTTCCCTTCTTCTCGCCACGTT 1929	
D1	216 ACTTGCCAGCGCGCTAGCGCGCGCTCTCTTTGCTTTCTTCCCTTCTTCTCGCCACGTT 2227	
Q1	193 CGCGGCTTTCCCGTCAAGCTCTAAATCGGGC- TCCCTTTAGGGTTCCGATTAAGTC 1988	
D1	222 CGCGGCTTTCCCGTCAAGCTCTAAATCGGGC- TCCCTTTAGGGTTCCGATTAAGTC 2287	
Q1	198 TTACGGCACTCGACCCCAAAACTTGATTAGGGTGATGTTTACGTAGTGGCCATC 2048	
D1	228 TTACGGCACTCGACCCCAAAACTTGATTAGGGTGATGTTTACGTAGTGGCCATC 2347	
Q1	204 GCGCTGTAGCGGTTTTTCCGCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGACT 2108	
D1	234 GCGCTGTAGCGGTTTTTCCGCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGACT 2407	
Q1	210 CTGTGTTCCAACTGGACACACTCAACCTATCTCGGTCTATCTTTGATTAAGG 2168	
D1	240 CTGTGTTCCAACTGGACACACTCAACCTATCTCGGTCTATCTTTGATTAAGG 2467	
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D1	246 GATTTGCGGATTTGCGGCTTATGTTTAAATAAGTCTGATTTTAAATAAATAAGC 2527	
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D1	258 CCGCAAGGCGAAGATGCAAGCATCATCTCAATTAGTCAGCAACACAGGTGGA 2639	
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D1	264 AGTCCCGAGGCTCCCGCAGGCGAAGATGCAAGCATCATCTCAATTAGTCAGCA 2699	
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D1	270 ACATAGTCCCGGCTTAACTCCGCCATCCCGCCCTAACTCCGCCAGTTCCGCCAT 2759	
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D1	293 CCATGATTGAACAAGATGGAATGCAAGGCTTTCTCCGGCGCTTGGGTGGAGGCTTA 2789	
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D1	3540 AATGGCGGCTTTTCTGATTCATCGACTGTGGCGGCTGGGTGGCGGACCG 3399	
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D1	3600 GACATAGCTTGCTACCGCTGATATTGCTGAAGACTTTGGCGGCAATGGGCT 3659	
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621 CACAGGAAATGTTGAATCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 6275  
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633 GGTTCGCGCACATTTCCCGGAAAGTGCCACCTGACGTC 6375  
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-69 B-4  
e 4 Application US/09646691B  
No. 5642353  
AL INFORMATION:  
APPLICANT: McCONNELL, Stephen, J. and SPINELLA, Dominic, G.  
TITLE OF INVENTION: PEPTIDE LIGANDS FOR THE ERYTHROPOIETIN  
RECEPTOR

NUMBER OF SEQUENCES: 90  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gen-Probe Incorporated  
STREET: 10210 Genetic Center Drive  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92121  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
FILING DATE: 20-Sep-2000  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Gritzmacher, Christine A  
REGISTRATION NUMBER: 40,627  
REFERENCE/DOCKET NUMBER: CB9701-A01  
TELEPHONE: 619-410-8926  
TELEFAX: 619-410-8928  
TELEX: <Unknown>

NAME FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6338 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
-69 B-4

Query Match 56.1%; Score 3578.4; DB 4; Length 6338  
Best Local Similarity 88.9%; Pred. No. 0;  
Matches 4141; Conservative 0; Mismatches 16; Indels 503; Gaps 5;  
QY 1750 GAGTCTCAGCTTTTCTGAGCGCGGAAAGAACAGCTGGGGCTCTAGGGGGTATC 1809  
Db 2148 GGGCTCTATGCTTCTGAGCGCGGAAAGAACAGCTGGGGCTCTAGGGGGTATC 2209  
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QY 3936 CGATTCCACCGCGCTTCTTATGAAGGTTGGGCTTCGGAAATCGTTTTCGGGGA |||  
Db 3899 CGATTCCACCGCGCTTCTTATGAAGGTTGGGCTTCGGAAATCGTTTTCGGGGA |||  
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Db 4019 TATTGCGAGCTTATTAATGGTTACAAATAAGCAATAGCATCAAAATTTCAAAA |||  
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Db 4079 ATTTTTCCTACGTCATTTCTAGTTGTGTGTGTTGTCCAAAATCTCATATGTATCTTA |||  
QY 4176 CTGTATACCGTFCGACCTCTAGCTAGAGCTTGGCGTAAATCATGTGCTCATAGCTGTT |||  
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QY 4356 TTTCCAGTTCGGGAAACCTGTGCTGCCAGCTGCTATTAATGAATCGGCCAAGCGGC |||  
Db 4319 TTTCCAGTTCGGGAAACCTGTGCTGCCAGCTGCTATTAATGAATCGGCCAAGCGGC |||  
QY 4416 AGGCGGTTTGGTATGGGGCTCTTCCGCTTCTCGCTCACTCACTCACTCGCTGGG |||  
Db 4379 AGGCGGTTTGGTATGGGGCTCTTCCGCTTCTCGCTCACTCACTCACTCGCTGGG |||  
QY 4476 CGTTCCGCTCGCGGAGCGGTATCAGCTCACTCAAAAGCGGTAAATPACGGTTATC |||  
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Db 4499 ATCAGGGGATTAACGAGGAAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAG |||  
QY 4596 TAAAAAGGCGCGGTTGCTGGCGTTTTCATAGGCTCCGCGCCCTCGACGAGCA |||  
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545. CCGAGTGTGCAATGATACCGGAGACCCACGCTCAGCGCTCCAGATTTATCAGCAAT 5518  
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551. AACCAGCAGCGGAGGCGCAGAGCTGAGTGTCTGCAACTTTATCCGCTCCAT 5578  
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563. CAGTGTGTTGCAATGCTACAGGATCTGTTGTCAGCTCGTCTGTTGGTAGGCTTC 5698  
573. ATTACAGTCCGGTTCCCAAGCAGTCAAGGCGAGTTACATGATCCCCCATGTTGTCAGAAA 5795  
569. ATTACAGTCCGGTTCCCAAGCAGTCAAGGCGAGTTACATGATCCCCCATGTTGTCAGAAA 5758  
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575. ACGGTTAGTCTCTCGGCTCTCCGATCGTTGTGAGAAGTAAGTTGGCGCAGTGTATC 5818  
585. ATTATGTTATGGCAGCAGTCAATTTCTTCTTATGTCATGCCATTCGCTAAGATGCTT 5915  
581. ATTATGTTATGGCAGCAGTCAATTTCTTCTTATGTCATGCCATTCGCTAAGATGCTT 5878  
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587. TTTCTGACTGTGGTACTCAACCAAGTCAATTCAGATAAGTATGCGGCGAG 5938  
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593. TTGCTCTTGC CGCGCTCAATACGGGATAATACCGGCCACATAGCAGAACTTTAAAGT 5998

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6239 GGGTTATTTCTCATGAGCGGATACATATTTGAATGTTATTAGAAAAATAAC 6298  
6336 GGTTCGCGCAGCATTTTCCCGAAAAAGTGCCACCTGACGTC 6375  
6299 GGTTCGCGCAGCATTTTCCCGAAAAAGTGCCACCTGACGTC 6338

## RESULT 5

US-09-796-575-3  
; Sequence 3, Application US/09796575  
; Patent No. 6632671  
; GENERAL INFORMATION:  
; APPLICANT: Genesegues, Inc.  
; TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD  
; FILE REFERENCE: G332.12-0001  
; CURRENT APPLICATION NUMBER: US/09/796,575  
; CURRENT FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: US 60/185,282  
; PRIOR FILING DATE: 2000-02-28  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 8578  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Supplied by Invitrogen of Carlsbad, California.  
US-09-796-575-3

Query Match 56.1%; Score 3578.4; DB 4; Length 8578;  
Best Local Similarity 88.9%; Pred. No. 0;  
Matches 4141; Conservative 0; Mismatches 16; Indels 503; gaps 5;  
QY 1750 GAGCTCCAGCTTTCTGAGCGGAAAGAACACAGCTGGGGCTCTAGGGGTATCC 1809  
DB 4388 GGGCTCTATGGCTTCTGAGCGGAAAGAACACAGCTGGGGCTCTAGGGGTATCC 4447  
QY 1810 GCCCTGTAGCGGCAATTAAAGCGCGCGGTGTGGTGTAGCGCGAGCGTGAC 1869  
DB 4448 GCCCTGTAGCGGCAATTAAAGCGCGCGGTGTGGTGTAGCGCGAGCGTGAC 4507  
QY 1870 ACTTGCAGCGGCTTAGCGCCCGCTCTTTCGTTTCTCCCTTCCTTTCTCGC 1929  
DB 4508 ACTTGCAGCGGCTTAGCGCCCGCTCTTTCGTTTCTCCCTTCCTTTCTCGC 4567  
QY 1930 CGCCGCTTTTCCCGCTCAGCTCTAAATCGGGGCTCCCTTTTAGGGTCCGATT 1988  
DB 4568 CGCCGCTTTTCCCGCTCAGCTCTAAATCGGGGCTCCCTTTTAGGGTCCGATT 4627  
QY 1989 TTTTAGCGCACCTCGACCCCAAAAACCTTGATTAGGGTGTGTTTACAGTAGTGG 2046  
DB 4628 TTTTAGCGCACCTCGACCCCAAAAACCTTGATTAGGGTGTGTTTACAGTAGTGG 4687  
QY 2049 GCCCTGTAGACGTTTTCGCCCTTTTGACGTTGAGTCCACGTTCTTTTAATAG 2104

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Q <sub>1</sub>	423	GTGAATTTGTTATCCCGCTCAAAATTCACACAAATACGAGCCGGAAGCATATAAGTGTAA	4291
D <sub>1</sub>	543	GTGAATTTGTTATCCCGCTCAAAATTCACACAAATACGAGCCGGAAGCATATAAGTGTAA	6498
Q <sub>2</sub>	429	AGCTCGGGTGCCTTAATGAGTGAGCTTAACCTCAATTAATTTGCTTGGCTCACTGCCCGC	4355
D <sub>2</sub>	649	AGCTCGGGTGCCTTAATGAGTGAGCTTAACCTCAATTAATTTGCTTGGCTCACTGCCCGC	6558
Q <sub>3</sub>	435	TTTCCAGTCCGGGAAACCTGTCTGTGCCACAGCTGCATTAAATGAATCGGCCAAACCGCCGGGAG	4415
D <sub>3</sub>	555	TTTCCAGTCCGGGAAACCTGTCTGTGCCACAGCTGCATTAAATGAATCGGCCAAACCGCCGGGAG	6618
Q <sub>4</sub>	441	AGCGGTTTCCGTATTGCGGCGCTCTTCGCGCTCTCTCGCTCACTGACTGCGCTGCGCTCGGT	4475
D <sub>4</sub>	561	AGCGGTTTCCGTATTGCGGCGCTCTTCGCGCTCTCTCGCTCACTGACTGCGCTGCGCTCGGT	6678
Q <sub>5</sub>	447	CGTTTCGCTCGCGGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATACGGTTATTCACAGA	4535
D <sub>5</sub>	567	CGTTTCGCTCGCGGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATACGGTTATTCACAGA	6738
Q <sub>6</sub>	453	ATCAGGCGGATAAACGACAGAAAGAACATGTGACAGAAAGGCGCAGCAAAAGGCCACAGGAACCG	4595
D <sub>6</sub>	673	ATCAGGCGGATAAACGACAGAAAGAACATGTGACAGAAAGGCGCAGCAAAAGGCCACAGGAACCG	6798
Q <sub>7</sub>	459	TAAAAGGCCGCGTTGTGCGGTTTTTCCATATAGCTCCGCCCCCTCGAAGCATCACAA	4655
D <sub>7</sub>	678	TAAAAGGCCGCGTTGTGCGGTTTTTCCATATAGCTCCGCCCCCTCGAAGCATCACAA	6858
Q <sub>8</sub>	465	AAATCGACGCTCAAGTCAGAGGTGGGGAACCGACAGGACTATAAGATACACAGCGTT	4715
D <sub>8</sub>	685	AAATCGACGCTCAAGTCAGAGGTGGGGAACCGACAGGACTATAAGATACACAGCGTT	6918
Q <sub>9</sub>	471	TCCCTCTGGAAGCTCCCTCGTGGCGCTCTCCTGTTTCGACCCCTCGCGCTTACCCGGATACCT	4775
D <sub>9</sub>	691	TCCCTCTGGAAGCTCCCTCGTGGCGCTCTCCTGTTTCGACCCCTCGCGCTTACCCGGATACCT	6978
Q <sub>10</sub>	477	GTCCGCTTTCTCCCTTCGGGAAAGCGTGGCGTTTTCTCATAGCTACGCTGTAGGTATCT	4835
D <sub>10</sub>	708	GTCCGCTTTCTCCCTTCGGGAAAGCGTGGCGTTTTCTCATAGCTACGCTGTAGGTATCT	7038
Q <sub>11</sub>	483	CAGTTCGGTGTAGGTGGTTCGCTCCAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCC	4895
D <sub>11</sub>	703	CAGTTCGGTGTAGGTGGTTCGCTCCAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCC	7098
Q <sub>12</sub>	489	CACCGCTCGGCTTATCCGGTAACTATCGCTTTGAGTCCAAACCGGTAAAGCACGACTT	4955
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Q <sub>13</sub>	495	ATCGCACTGGCAGCAGCCACTGGTAAACAGATTACAGAGCGAGGTATGTAGCGGCTGC	5015
D <sub>13</sub>	715	ATCGCACTGGCAGCAGCCACTGGTAAACAGATTACAGAGCGAGGTATGTAGCGGCTGC	7218
Q <sub>14</sub>	501	TACAGAGTTCCTCAAGTGTGGCTTAACCTACGCTACACTAGAAAGACAGTATTGGTAT	5075
D <sub>14</sub>	721	TACAGAGTTCCTCAAGTGTGGCTTAACCTACGCTACACTAGAAAGACAGTATTGGTAT	7278
Q <sub>15</sub>	507	CTCGGCTCTGCTGAAGCCAGTTACTTTCGGAAAAAGAGTTGGTAGCTCTTTGATCCGGCAA	5135
D <sub>15</sub>	727	CTCGGCTCTGCTGAAGCCAGTTACTTTCGGAAAAAGAGTTGGTAGCTCTTTGATCCGGCAA	7338
Q <sub>16</sub>	513	CAAAACACCGCTGGTAGCGGTGGTTTTTTTGTTCGAAAGACAGATTACGCGCAGAAA	5195
D <sub>16</sub>	733	CAAAACACCGCTGGTAGCGGTGGTTTTTTTGTTCGAAAGACAGATTACGCGCAGAAA	7398
Q <sub>17</sub>	519	AAAGGATCTCAAGAGATCCTTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGA	5255
D <sub>17</sub>	738	AAAGGATCTCAAGAGATCCTTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGA	7458
Q <sub>18</sub>	525	AACTCAGCTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACTTAGATCCT	5315
D <sub>18</sub>	745	AACTCAGCTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACTTAGATCCT	7518
Q <sub>19</sub>	531	TTTAAATTTAAATTAAGATTTTAAATCTTAAAGTATATATGAGTAAACTTTGGTCTGA	5375

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Db	5940	ACCATAGTCCCGCCCTTAACTCTCGGCCCATCCCGCCCTTAACCTCCGCCCCAGTTCC
Qy	2528	TCTTCGCGCCCATGCGCTGACTAATATTTTTTTTATTTATGCGAGAGCGCGAGGCGCGC
Db	6000	TCTTCGCGCCCATGCGCTGACTAATATTTTTTTTATTTATGCGAGAGCGCGAGGCGCGC
Qy	2588	TCTTGAGCTATTCGACGAAGTAGTGCAGAGGCTTTTTTTGGAGGCCCTAGGCTTTTTCG
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Qy	2676	CGCATGATGAAACAAGATGGATTGCAAGCAGGTTCTCCGGCCGCTTTGGGTGGAG
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Db	6240	TTCGGCTATGACTGGGCAACAACAGACAACTCGGCTGCTCTGATGCCGCCGCTGTTTC
Qy	2796	TCAGCGAGGGGCGCCCGGTTCTTTTGTGTCAGAACCGAAGCTGTGCCGGTGCCTCG
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Qy	2856	CTGCAAGACGAGGACAGCGCGCTATCTGCGCTGGCCACAGACGGGCGCTTCCTTCG
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Qy	2916	GTGCTCGACGTTGTCACTGAAGCGGAAGGACTGGCTGCTATTTGGGCGCAAGTG
Db	6420	GTGCTCGACGTTGTCACTGAAGCGGAAGGACTGGCTGCTATTTGGGCGCAAGTG
Qy	2976	CAGGATCTCGTGTCTCATCTGCTTCCTGCGGAGAAAGTATCCATCATGGCT
Db	6480	CAGGATCTCGTGTCTCATCTGCTTCCTGCGGAGAAAGTATCCATCATGGCT
Qy	3036	ATCGCGCGGCTGCATACGTTTGATTCGGGCTACTCTGCCCATTCGACCAACCAAGCG
Db	6540	ATCGCGCGGCTGCATACGTTTGATTCGGGCTACTCTGCCCATTCGACCAACCAAGCG
Qy	3096	CGCATCGAGCGACACGTACTCGGATGGAAGCCGGTCTGTGTCATCAGGATGAT
Db	6600	CGCATCGAGCGACACGTACTCGGATGGAAGCCGGTCTGTGTCATCAGGATGAT
Qy	3156	GAAGAGCATCAGGGGCTCGCGCCAGCGGAACCTGTTCGCAGGCTCAAGGCGAGC
Db	6660	GAAGAGCATCAGGGGCTCGCGCCAGCGGAACCTGTTCGCAGGCTCAAGGCGAGC
Qy	3216	GACGGGAGGAATCTCGTGTGTGACCCATGGCGATGCTGTTCGCGGAATATCATG
Db	6720	GACGGGAGGAATCTCGTGTGTGACCCATGGCGATGCTGTTCGCGGAATATCATG
Qy	3276	AATGGCCGCTTTTCTGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGC
Db	6780	AATGGCCGCTTTTCTGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGC
Qy	3336	GACATAGCGTTGGCTACCGCTGATATTTGCTGAAGAGCTTTGGCGGCGAATGGGCT
Db	6840	GACATAGCGTTGGCTACCGCTGATATTTGCTGAAGAGCTTTGGCGGCGAATGGGCT
Qy	3396	TTCTCTGTGTGCTTTACGATTCGCGCTCCCGATTTGCGAGGCAATCGCCTTCTAT
Db	6900	TTCTCTGTGTGCTTTACGATTCGCGCTCCCGATTTGCGAGGCAATCGCCTTCTAT
Qy	3456	CTTGACGAGTTCTTCTTGAGCGGCACTCTGGGTTTCGAAATGACCGGACCAAGCGA



D1: 596 CTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTGGAATGACCGACCAAGCAGCGCCCA 7019  
Q1: AACTGGCATCAGAGATTTCGATTCCACCGCCGCTCTTATGAAGGTTGGGCTTCGAA 3575  
D1: 702 AACTGGCATC----- 7029  
Q1: TCGTTTCCGGGACCGCGCTGGATGATCTCCAGCGCGGGATCTCATGCTGGAGTTCT 3635  
D1: 703 ----- 7029  
Q1: TCGCCACCTTAGGGGAGGCTAACTGAACAACGGAAGGAGACAATACCGAAGGAACCC 3695  
D1: 703 ----- 7029  
Q1: GGCATGACGGCAATAAAGACAGATAAAGACGAGTGTGGGTGCTTGTTCATAA 3755  
D1: 703 ----- 7029  
Q1: ACGGGGTTGGTCCAGGGCTGGCACTCTGTGATACCCACCGAGACCCCATTTGGGG 3815  
D1: 703 ----- 7029  
Q1: CAAATAGCGCGGTTTCTTCTTTCCACCCACCCCGCAAGTTTCGGGTGAAGSCCC 3875  
D1: 703 ----- 7029  
Q1: AAGGCTGCGAGCCAAAGTGGGGCGGAGCGCCCTGCCATAGCCTCAGTGTACGAGATTT 3935  
D1: 703 -----ACGAGATTT 7038  
Q1: GATTCCACCGCGCCTTCTATGAAGTTTGGGCTTCGGAATCGTTTTCGGGACGCGG 3995  
D1: 703 CATTCCACCGCGCCTTCTATGAAGTTTGGGCTTCGGAATCGTTTTCGGGACGCGG 7098  
Q1: TGGATGATCTCTCAGCGCGGATCTCATGTGGAGTTCTTCGCCACCCCAACTTTGT 4055  
D1: 709 TGGATGATCTCTCAGCGCGGATCTCATGTGGAGTTCTTCGCCACCCCAACTTTGT 7158  
Q1: TATTGAGCTTATAATGGTTTACAAATAAAGCAATAGCATCACAAATTTTCAAAATAAGC 4115  
D1: 715 TATTGAGCTTATAATGGTTTACAAATAAAGCAATAGCATCACAAATTTTCAAAATAAGC 7218  
Q1: ATTTTTCACGCACTTAGTTGTGGTTGTTCGCAACTCATATGTATCTTATCATGT 4175  
D1: 721 ATTTTTCACGCACTTAGTTGTGGTTGTTCGCAACTCATATGTATCTTATCATGT 7278  
Q1: CTGTATACCGTCCAGCTCTAGCTAGAGCTTGGGTTAATCATGTCTATGCTGTTTCTGT 4235  
D1: 727 CTGTATACCGTCCAGCTCTAGCTAGAGCTTGGGTTAATCATGTCTATGCTGTTTCTGT 7338  
Q1: GTGAATTTGTTATCCGCTCAAAATTCACACATACGAGCGGAAGCATAAAGTGTA 4295  
D1: 733 GTGAATTTGTTATCCGCTCAAAATTCACACATACGAGCGGAAGCATAAAGTGTA 7398  
Q1: ABCTCGGGTCTTAATGATGAGCTTAATCAATTAATTTGGCTTGGCTCACTGCCCCG 4355  
D1: 739 ABCTCGGGTCTTAATGATGAGCTTAATCAATTAATTTGGCTTGGCTCACTGCCCCG 7458  
Q1: TTTCCAGTCGGGAAACCTGTGTGCGCAGCTGCAATTAATGAATCGGCCAACCGCGGGAG 4415  
D1: 745 TTTCCAGTCGGGAAACCTGTGTGCGCAGCTGCAATTAATGAATCGGCCAACCGCGGGAG 7518  
Q1: ACGGGTTGGGATTTGGGGCTCTTCCGGTTCCTCGCTCACTGACTGCTGCTGCGCTCGGT 4475  
D1: 751 ACGGGTTGGGATTTGGGGCTCTTCCGGTTCCTCGCTCACTGACTGCTGCTGCGCTCGGT 7578  
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D1: 757 CTTTCGGCTCGGGAGCGGTATCAGCTCACTCAAGGGGTTAATACGTTATCCACAGA 7638  
Q1: ATCAGGGGATACCGCAGGAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCG 4595  
D1: 763 ATCAGGGGATACCGCAGGAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCG 7698

Q1: 4596 TAAAAAGGCGCGCTTGTCTGGCGTTTTTTCATAGGCTCCGCCCTCGACGAGCTTACAA 4655  
D1: 7699 TAAAAAGGCGCGCTTGTCTGGCGTTTTTTCATAGGCTCCGCCCTCGACGAGCTTACAA 7758  
Q1: 4656 AATTCAGCGCTCAAGTCAGAGTGGGGAACCCGACAGGACTATAAGATACCT 4715  
D1: 7759 AATTCAGCGCTCAAGTCAGAGTGGGGAACCCGACAGGACTATAAGATACCT 7818  
Q1: TCCCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCGAGCCCTCGCGCTTACCG 4775  
D1: 7819 TCCCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCGAGCCCTCGCGCTTACCG 7878  
Q1: GTCCGCTTTTCTCCCTTCGGAAGCGTGGCGCTTCTCTATAGCTCAGCTGTAT 4835  
D1: 7879 GTCCGCTTTTCTCCCTTCGGAAGCGTGGCGCTTCTCTATAGCTCAGCTGTAT 7938  
Q1: 4836 CAGTTCCGTTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGACAGAACCCCGCT 4895  
D1: 7939 CAGTTCCGTTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGACAGAACCCCGCT 7998  
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D1: 7999 CGACCGCTGGCGCTTATCCGTTAACTATCTGTCTTGTAGTCCAAACCCCGTAAGCT 8058  
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D1: 8059 ATCGCCACTGGCAGCAGCCACTGTTAAACAGGATTAGCAGCGGAGGTATGTAG 8118  
Q1: 5016 TACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACCTAGGAACAGTAT 5075  
D1: 8119 TACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACCTAGGAACAGTAT 8178  
Q1: 5076 CTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGTTGGTAGCTCTTGATC 5135  
D1: 8179 CTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGTTGGTAGCTCTTGATC 8238  
Q1: 5136 ACAACCCAGCGCTGGTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATACCGC 5195  
D1: 8239 ACAACCCAGCGCTGGTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATACCGC 8296  
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D1: 8299 AAAGGATCTCAAGAGATCTTTTGTATCTTTTCTACGGGCTCGAGCTCAGTC 8358  
Q1: 5256 AAATCAGCTTAAGGATTTTGGTCATGAGATTATCAAAAGGATCTTCACCT 5315  
D1: 8359 AAATCAGCTTAAGGATTTTGGTCATGAGATTATCAAAAGGATCTTCACCT 8418  
Q1: 5316 TTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 5375  
D1: 8419 TTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT 8478  
Q1: 5376 CAGTTACCAATGCTTAATCAGTGAGGACCTATCTCAGGATCTGTCTATTTCG 5435  
D1: 8479 CAGTTACCAATGCTTAATCAGTGAGGACCTATCTCAGGATCTGTCTATTTCG 8538  
Q1: 5436 CATAGTTGCTGACTCCCGCTCGTGTAGATACTACGATACGGAGGGCTTACC 5495  
D1: 8539 CATAGTTGCTGACTCCCGCTCGTGTAGATACTACGATACGGAGGGCTTACC 8598  
Q1: 5496 CCCCAGTGTGCAATGATACCGCGAGACCCAGCTCACGGCTCCAGATTTATC 5555  
D1: 8599 CCCCAGTGTGCAATGATACCGCGAGACCCAGCTCACGGCTCCAGATTTATC 8658  
Q1: 5556 AAACCGAGCAGCGCGGAGGGCGGAGAGTGGTCTCTGCAACTTTTATCCGC 5615  
D1: 8659 AAACCGAGCAGCGCGGAGGGCGGAGAGTGGTCTCTGCAACTTTTATCCGC 8718  
Q1: 5616 CCAGTCTATTATTTGTTGCGGGAGAGTAGTAGTAGTTCCGCCAGTTAAATAG 5675  
D1: 8719 CCAGTCTATTATTTGTTGCGGGAGAGTAGTAGTAGTTCCGCCAGTTAAATAG 8778

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 AGTTGTTGCCATTGCTACAGCATCGTGGTGTCAAGCTCGTGGTGTGGTATGGCTTC 8838  
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 GCTCTTGGCCGCGCTCAATACGGGATAATACCGGCCACATAGCAGAACTTTTAAAGT 9138  
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 TTCCGCGCAATTTCCCGAAGTCCACCTGACGTC 6375  
 TTCCGCGCAATTTCCCGAAGTCCACCTGACGTC 9478

plication US/08741881  
 9245

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VENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS

SEQUENCES: 128

NCE ADDRESS:

: SEED and BERRY LLP  
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04-7092

ADABLE FORM:

PE: Floppy disk

IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA: US/08741,881  
 APPLICATION NUMBER: US/08741,881  
 FILING DATE: 30-OCT-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McMaisters, David D.  
 REGISTRATION NUMBER: 33,963  
 REFERENCE/DOCKET NUMBER: 930049.42306 / 1146.007  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 682-6031  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16656 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-741-881-1

Query Match 56.1%; Score 3578.4; DB 1; Length 16656  
 Best Local Similarity 88.9%; Pred. No. 0;  
 Matches 4141; Conservative 0; Mismatches 16; Indels 503;

QY 1750 GAGCTCCAGCTTTTCTGAGCGGAAAGAACCCAGCTGGGGCTCTAGGGGGTATCC  
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 QY 1810 GCCCTGAGCGGCGCATTAAGCGCGGGGTGTGGTGTACGCGCAGCGTGAC  
 DB 12059 GCCCTGAGCGGCGCATTAAGCGCGGGGTGTGGTGTACGCGCAGCGTGAC  
 QY 1870 ACTTGGCAGCGCCCTAGCGCGCGCTTCTTGGCTTCTTCCCTTCTTCTCGC  
 DB 12119 ACTTGGCAGCGCCCTAGCGCGCGCTTCTTGGCTTCTTCCCTTCTTCTCGC  
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 DB 12179 CGCCGGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTAGGGTTCCGATT  
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 DB 12239 TTTACGGCAGCTCGACCCCAAAAACTTGATAGGGGTGATGGTTCACGATGCG  
 QY 2049 GCCCTGATAGCAGGTTTTCGCCCTTTGACGTTGCGAGTCCACGTTCTTTAATAG  
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 QY 2109 CTCTGTTCCAAACTGGAACCAACCTCAACCTTATCTCGTCTTATTTTGTATTT  
 DB 12359 CTCTGTTCCAAACTGGAACCAACCTCAACCTTATCTCGTCTTATTTTGTATTT  
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 QY 2349 CCCCCAGGAGATGATGCAAGCATGCAATCTCAATTAGTCAGCAACGAGG  
 DB 12531 CCCCCAGGAGGAGATGATGCAAGCATGCAATCTCAATTAGTCAGCAACGAGG  
 QY 2408 AAGTCCCCAGGCTCCCCAGCAGGAGGATGATGCAAGCATGCAATCTCAATTAG  
 DB 12591 AAGTCCCCAGGCTCCCCAGCAGGAGGATGATGCAAGCATGCAATCTCAATTAG

Q1	246	A	CCATAGTCCGCGCCCTAACTCCGCCCATCCGCGCCCTAACTCCGCCAGATTCCGCCCAT	2527
D1	264	A	CCATAGTCCGCGCCCTAACTCCGCCCATCCGCGCCCTAACTCCGCCAGATTCCGCCCAT	12710
Q1	252	T	CTCCGCGCCCATGGCTGACTAAATTTTTTTTATTTATGACAGCGCCGAGCGCGCTTCGCGC	2587
D1	271	T	CTCCGCGCCCATGGCTGACTAAATTTTTTTTATTTATGACAGAGCCGAGCGCGCTTCGCGC	12770
Q1	258	T	CTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCGCTAGGCTTTTTGCAAAAGAT	2647
D1	277	T	CTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCGCTAGGCTTTTTGCAAAAG	12830
Q1	266	C	-----GATCAAGACAGACAGGATGAGGATCGTTT	2675
D1	283	C	CTCCGCGAGCTGTATATCCATTTTCGGATCTGATCAAGACAGGATGAGGATCGTTT	12890
Q1	267	C	GCATGATTGAAACAAGATGGATTGCACGACAGTTCTCCGCGCGCTTGGTGAGAGGCTA	2735
D1	289	C	GCATGATTGAAACAAGATGGATTGCACGACAGTTCTCCGCGCGCTTGGTGAGAGGCTA	12950
Q1	273	T	TCGGCTATGACTGGGCAACAACAGACAATCGGCTGCTCTGATGCGCGCGTGTTCGGCTG	2795
D1	295	T	TCGGCTATGACTGGGCAACAACAGACAATCGGCTGCTCTGATGCGCGCGTGTTCGGCTG	13010
Q1	279	T	TCAGCGACGGGCGCGCGTCTTTTTGTCAAGACGACCTGTCCGGTGCCCTGAATGAA	2855
D1	301	T	TCAGCGACGGGCGCGCGTCTTTTTGTCAAGACGACCTGTCCGGTGCCCTGAATGAA	13070
Q1	285	C	TCGACAGACGAGCGCGGCGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGGCAGCT	2915
D1	307	C	TCGACAGACGAGCGCGGCGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGGCAGCT	13130
Q1	291	G	TGCTCGACGCTTGCTCACTGAAGCGGAAAGGACTGGCTGCTATTGGCGGAAGTGCCGGG	2975
D1	313	G	TGCTCGACGCTTGCTCACTGAAGCGGAAAGGACTGGCTGCTATTGGCGGAAGTGCCGGG	13190
Q1	297	C	AGGATCTCTGTCACTCACTTGCTCTCTGCGGAAAGTATCCATCATGCTGAATGCA	3035
D1	319	C	AGGATCTCTGTCACTCACTTGCTCTCTGCGGAAAGTATCCATCATGCTGAATGCA	13250
Q1	303	A	TGCGGCGGCTGATACGCTTGATCGGCTACTCGGCCCATTCGACCAACAGCGAAACAT	3095
D1	325	A	TGCGGCGGCTGATACGCTTGATCGGCTACTCGGCCCATTCGACCAACAGCGAAACAT	13310
Q1	309	C	GCATCGAGCGACACGTAATCGGATGGAAGCGGCTTGTCGATCAGATGATCTGGAC	3155
D1	331	C	GCATCGAGCGACACGTAATCGGATGGAAGCGGCTTGTCGATCAGATGATCTGGAC	13370
Q1	315	G	AGAGCATCAGGGGCTCGCGCAGCGAACTTGTCGACAGCTCAAGCGCAGCATGCCC	3215
D1	337	G	AGAGCATCAGGGGCTCGCGCAGCGAACTTGTCGACAGCTCAAGCGCAGCATGCCC	13430
Q1	321	G	AGCGCGAGCATCTCGTGTGACCCATGGGATGCTGCTTGCCGAAATCATGCTGAA	3275
D1	343	G	AGCGCGAGCATCTCGTGTGACCCATGGGATGCTGCTTGCCGAAATCATGCTGAA	13490
Q1	327	A	ATGGCGCGCTTTTCTGGAATTCATCGACTGTGGCGGCTGGGTGTGGCGACCGCTATCAG	3335
D1	349	A	ATGGCGCGCTTTTCTGGAATTCATCGACTGTGGCGGCTGGGTGTGGCGACCGCTATCAG	13550
Q1	333	C	ACATAGCGTTCGCTACCGCTGATATGCTGAAGAGCTTTGGCGGCAATGGGCTGACCGC	3395
D1	355	C	ACATAGCGTTCGCTACCGCTGATATGCTGAAGAGCTTTGGCGGCAATGGGCTGACCGC	13610
Q1	339	T	TCTCTGCTGCTTTACGGTATCGCGCTCCCGATTGCGACGGCATCGCTTTCTATCGCCTT	3455
D1	361	T	TCTCTGCTGCTTTACGGTATCGCGCTCCCGATTGCGACGGCATCGCTTTCTATCGCCTT	13670
Q1	345	C	TTGACGAGTTCCTCTGAGCGGAGCTCTGGGTTTGGAAATGACCGACCAAGCGAGGCCA	3515
D1	367	C	TTGACGAGTTCCTCTGAGCGGAGCTCTGGGTTTGGAAATGACCGACCAAGCGAGGCCA	13730
Q1	351	A	ACTTGCCATCAAGAGATTTGATTTCAACCGCGCGCTTCTATGAAGTTGGGCTTCGAA	3575

13731		ACCTGCCATC-----	-----	13740
3576	TCGTTTCCGGGACCGCGCTGGATGATCCTCAGCGCGGGGATCTCATGCTGC	-----	-----	3635
13741	-----	-----	-----	13740
3636	TCGCCACCCTAGGGGAGGCTAACTGAACACGGAAGGAGACAATACCGAAC	-----	-----	3645
13741	-----	-----	-----	13740
3696	CGCATGACGGCAATAAAAAAGACAGAATAAAACGACGGTGTGGGTGGTTTG	-----	-----	3715
13741	-----	-----	-----	13740
3756	ACGCGGGTTTCGGTCCAGCGGCTGGCACTCTGTGATACCCACCGAGACCCCT	-----	-----	3815
13741	-----	-----	-----	13740
3816	CCAATACGCGCGGTTTCTTCCTTTTCCCAACCCACCCCAAGTTGGGTG#	-----	-----	3875
13741	-----	-----	-----	13740
3876	AGGCTCGACGCCAAAGTCCGGGCGCAGGCCCTGCCATAGCCTCAGTGTACC	-----	-----	3935
13741	-----	-----	-----	13749
3936	CGATTCCACCGCGCCTTCTATGAAGGTTGGCTTCGGAATCGTTTTCGGGP	-----	-----	3985
13750	CGATTCCACCGCGCCTTCTATGAAGGTTGGGCTTCGGAATCGTTTTCGGGP	-----	-----	13809
3996	CTGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCGCCCAACCCCA	-----	-----	4055
13810	CTGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCGCCCAACCCCA	-----	-----	13869
4056	TATTGCAGCTTAATAATGTTTCAAAATAAGCAATAGCATCAAAATTTCACAAF	-----	-----	4115
13870	TATTGCAGCTTAATAATGTTTACAAATAAGCAATAGCATCAAAATTTCACAAF	-----	-----	13929
4116	ATTTTTTTCACGATCTAGTTGTGGTTGTGCCAACTCATCAATGATCTTA	-----	-----	4175
13930	ATTTTTTTCACGATCTAGTTGTGGTTGTGCCAACTCATCAATGATCTTA	-----	-----	13989
4176	CTGTATACCGTGCACCTTAGCTAGAGCTTGGCGTAATCATGTCATAGCTGT	-----	-----	4235
13990	CTGTATACCGTGCACCTTAGCTAGAGCTTGGCGTAATCATGTCATAGCTGT	-----	-----	14049
4236	GTGAAATTGTTATCCGCTCAAAATCCACACACATACGAGCCGGAAGCATAA	-----	-----	4295
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4296	AGCCTGGGTTGCCCTAATGATGAGCTAACTCATCAATTAATGGTTGCGCTACT	-----	-----	4355
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4356	TTTCCAGTCCGGAAACTGTGTCGCCAGTGCATTAATGAATCGGCCAACCGCG	-----	-----	4415
14170	TTTCCAGTCCGGAAACTGTGTCGCCAGTGCATTAATGAATCGGCCAACCGCG	-----	-----	14229
4416	AGCGGTTTCGTTATGGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTGCG	-----	-----	4475
14230	AGCGGTTTCGTTATGGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTGCG	-----	-----	14289
4476	CGTTCGCTCCGGGAGCGGTATCAGCTCACTCAAAGCGGTATATACGGTTATC	-----	-----	4535
14290	CGTTCGCTCCGGGAGCGGTATCAGCTCACTCAAAGCGGTATATACGGTTATC	-----	-----	14349
4536	ATCAGGGGATAACGACGAGAAAGCAATGTAGCAAAAGCCAGCAAAAGCCAG	-----	-----	4595
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TAGTTGCTGATCTCCCGCTGTGTAGATAACTACGATACGAGGCTTACCATCTGG 15309  
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ACCGCAGCGGAGGCGGAGCGAGAGTGGTCTCGAACTTTATCCGCTCCAT 5615  
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## RESULT 8

US-08-739-158-1  
; Sequence 1, Application US/08739158  
; Patent No. 5814482  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTE  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/739,158  
; FILING DATE: 30-OCT-1996  
; CLASSIFICATION: 514

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/ REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16656 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-739-167-1

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Query Match 56.1%; Score 3578.4; DB 2; length 16656
Best Local Similarity 88.9%; Pred. No. 0;
Matches 4141; Conservative 0; Mismatches 16; Indels 503; gaps 5;

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DB 11999 GGGCTCTATGGCTTCTGAGCGCGAAAGAACACGCTGCGGCTCTAGGGGGTATCC 13058
QY 1810 GCGCTGTAGCGCGCAATTAAAGCGCGCGGTGTGGTGTACGCGCAGCGTGAC 1869
DB 12059 GCGCTGTAGCGCGCAATTAAAGCGCGCGGTGTGGTGTACGCGCAGCGTGAC 12118
QY 1870 ACTTGCCAGCGCGCTAGCGCGCGCTCTTTCGCTTTCTTCCCTTCTTCTCGC 1929
DB 12119 ACTTGCCAGCGCGCTAGCGCGCGCTCTTTCGCTTTCTTCCCTTCTTCTCGC 12178
QY 1930 CGCGCGCTTTCCCGCTCAAGCTCTAATCGGGG-TCCTTTTAGGGTTCGGAT 1988
DB 12179 CGCGCGCTTTCCCGCTCAAGCTCTAATCGGGGATCCCTTTAGGGTTCGGAT 12238
QY 1989 TTTACGGCACTCGACCCCAAAAACCTTCATTAGGGTGTGGTGTACGCTAGTGC 2048
DB 12239 TTTACGGCACTCGACCCCAAAAACCTTCATTAGGGTGTGGTGTACGCTAGTGC 12298
QY 2049 GCGCTGATAGCGGTTTTTCGCGCTTTGAGTGTGGAGTCCAGCTTCTTTAATAG 2168
DB 12299 GCGCTGATAGCGGTTTTTCGCGCTTTGAGTGTGGAGTCCAGCTTCTTTAATAG 12358
QY 2109 CTTGTTCCAAACTGGACCAACTCAACCTATCTCGGTCTATTCTTTGATT 2168
DB 12359 CTTGTTCCAAACTGGACCAACTCAACCTATCTCGGTCTATTCTTTGATT 12418
QY 2169 GATTTGCGGATTTTCGCGCTATTGGTTAAAAATAGCTGATTAACAAAAAT 2228
DB 12419 GATTTGCGGATTTTCGCGCTATTGGTTAAAAATAGCTGATTAACAAAAAT 12478
QY 2229 GAATTAATTTCTGTGGAATGCCCGGAGCTTGTATATCCATTTTCGGATCTGATC 2228
DB 12479 GAATTAATTTCTGTGGAATGCCCGGAGCTTGTATATCCATTTTCGGATCTGATC 12487
QY 2289 GAGCGGAAAGAACACGCTGTGGAATGTGTGTCAGTTAGGGTGTGAAAGTCC 2346
DB 12488 -----CTGTGGAATGTGTGTCAGTTAGGGTGTGAAAGTCC 12510
QY 2349 CCCCCA-GCAGGCAGAGTATGCAAAAGCATGCAATCAATAGTCAACACACG 2407
DB 12531 CCCCCAGGCAGAGTATGCAAAAGCATGCAATCAATAGTCAACACACG 12590
QY 2408 AAGTCCCCAGGCTCCCCAGCAGGAGAGTATGCAAAAGCATGCAATCAATAG 2467
DB 12591 AAGTCCCCAGGCTCCCCAGCAGGAGAGTATGCAAAAGCATGCAATCAATAG 12650
QY 2468 ACCATAGTCCCGCCCTTAATCCCGCCATCCCGCCCTTAATCCCGCCATGTTCC 2527
DB 12651 ACCATAGTCCCGCCCTTAATCCCGCCATCCCGCCCTTAATCCCGCCATGTTCC 12710
QY 2528 TCTCCGCCCATGCGCTGACTAATTTTTTTTTTTTATGAGAGGCGGAGCGCC 2587
DB 12711 TCTCCGCCCATGCGCTGACTAATTTTTTTTTTTTATGAGAGGCGGAGCGCC 12770
QY 2588 TCTGAGCTATTCAGAGAGTAGTGAGGAGGCTTTTTTTGGAGGCGCTAGGCTTTTGC 2647

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Qy 3876 AGGCTCGACGCAACGTCGGGGCGGCGGCCCTGCCATAGCTCAGTGTCTAG  
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F A]		Email: watsonrj@agr.gc.ca.
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4a	R	Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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mays subsp. mays (maize)  
mays subsp. mays  
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bases 1 to 996)  
ti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,  
ard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.  
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blished (2003)

act: Bharti,A.K.  
oachim Messing's lab  
Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
ersity  
Frelinghuysen Road, Piscataway, NJ 08854, USA  
732 445 3801  
732 445 5735  
l: bharti@waksman.rutgers.edu  
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High quality sequence start: 11.  
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CK287930

LOCUS  
DEFINITION

CK287930 910 bp mRNA linear EST  
EST750652 Nicotiana benthamiana mixed tissue cDNA library  
normalized, full-length Nicotiana benthamiana cDNA clone  
end, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Other ESTs: EST750653

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

1..910

/organism="Nicotiana benthamiana"

/mol\_type="mRNA"

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/clone="NBMEC75"

/tissue type="abiotic and biotic stress-treated"

callus tissue and root tissue"

/lab host="DH10B-Tona"

/clone\_lib="Nicotiana benthamiana mixed tissue"

library, normalized, full-length"

/note="Vector: pCMVSPORT6.1; Site\_1: EcoRI; Site\_2: EcoRI"

supplier: RNA was isolated from Nicotiana benthamiana

tissues that include callus, roots from liquid

grown plants, heat-stressed leaves (38 C, 3 hr

cold-stressed leaves (5 C 3 hr, 6hr), and patho-

challenged leaves (Pseudomonas syringae pv toma-

Xanthomonas campestris pv campestris 12 hr, 18h

Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas

campestris pv vesicatoria 18hr). RNA was isolated

these tissues and pooled in approximately equal

amounts."

FEATURES

source

ORIGIN

Query Match 14.2%; Score 903.8; DB 14; Length 910;  
Best Local Similarity 99.8%; Pred. No. 5e-134;  
Matches 905; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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 bases 1 to 936)  
 l.C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.  
 ration of ESTs from potato callus tissue  
 blished (2003)  
 act: Robin Buell  
 Institute for Genomic Research  
 Medical Center Dr, Rockville, MD 20850, USA  
 l: potato-array@tigr.org  
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 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 1025)  
 AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A  
 Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.  
 Sequencing of the maize genome at PGIR (2003c)  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Bharti,A.K.  
 Dr.Joachim Messing's lab  
 The Plant Genome Initiative at Rutgers, Waksman Institut  
 University  
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
 Tel: 732 445 3801  
 Fax: 732 445 5735  
 Email: bharti@waksman.rutgers.edu  
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180: AAGGCGACAGCAAAATGTTGAATCATATCTTCTTTTCAATATTTGAAGCATTT 127
327: TATCAGGCTTATGCTCTATGAGCGGATACATATTTGAATGATTTAGAAAATAACAA 6330
126: TATCAGGCTTATGCTCTATGAGCGGATACATATTTGAATGATTTAGAAAATAACAA 67
331: AAGGGTTCGCGCATTTCCCGGAAAGTGCCACCTGA 6371
66: AAGGGTTCGCGCATTTCCCGGAAAGTGCCACCTAA 26

(234786 935 bp mRNA linear EST 15-DEC-2003
1: 5'GT47508 Nicotiana benthamiana mixed tissue cDNA library,
2: full-length, full-length Nicotiana benthamiana cDNA clone NBMAQ41 5',
3: cDNA mRNA sequence.
(234786
1: 5'GT4786.1 GI:39858698
2:
3:
4: Nicotiana benthamiana
5: Nicotiana benthamiana
6: Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
7: Eumatophyta; Magnoliophyta; eudicotyledons; core eudicots;
8: Geraniales; Lamiales; Solanales; Solanaceae; Nicotiana.
9: Bases 1 to 935)
10: Eick, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
11: Skaskawicz, B., Jin, H. and Baker, B.
12: Generation of EST sequences from Nicotiana benthamiana
13: Unpublished (2003)
14: Contact: Robin Buell
15: E-mail: ESR747509
16: The Institute for Genomic Research
17: 912 Medical Center Dr, Rockville, MD 20850, USA
18: E-mail: potato-array@tigr.org
19: Genes can be requested from TIGR via potato@tigr.org
20: E-mail primer: ATT TAG GTG ACA CTA TAG.
21: Location/Qualifiers
22: 1. .935
23: /organism="Nicotiana benthamiana"
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27: /tissue_type="abiotic and biotic stress-treated leaves,
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30: /clone_lib="Nicotiana benthamiana mixed tissue cDNA
31: library, normalized, full-length"
32: /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
33: supplier: RNA was isolated from Nicotiana benthamiana
34: tissues that include callus, roots from liquid culture
35: grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
36: cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
37: challenged leaves (Pseudomonas syringae pv tomato 12 hr;
38: Xanthomonas campestris pv campestris 12 hr, 18hr;
39: Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
40: campestris pv vesicatoria 18hr). RNA was isolated from
41: these tissues and pooled in approximately equal molar

```

ORIGIN	amounts."
Query Match	14.4%; Score 915.4; DB 14; Length 935;
Best Local Similarity	99.4%; Pred. No. 7.1e-136;
Matches 919; Conservative 0; Mismatches 6; Indels 0;	
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QY	2778 GCGCGCGTGTTCGGGCTGTACGGCAGGGGCGCGCGTTCTTTTTGTCAAGACC
DB	131 GCGCGCGTGTTCGGGCTGTACGGCAGGGGCGCGCGTTCTTTTTGTCAAGACC
QY	2838 TCCGGTGGCTGAATGAACCTGCAAGACGAGGCGCGGCTATCGTGCGCTGGCC
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QY	2958 TTGGGCGAAGTCCGGGCGAGGATCTCTGTCTCATCTCACTTGTCTCTGCCGAG
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QY	3078 GACCACCAAGCAAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAAGCCGGT
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DB	611 CCGAATATCATGTTGGAAATGGCGGCTTTCTGATTCATCGACTGTGGCGCGG
QY	3318 GTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGCTGATATTGCTGAAGAG
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DB	851 CCGACCAAGCGAGGCCCAACTGCCATCAGAGATTTTCGATTCCACCGCCGCTT
QY	3558 AAAAGTTGGGCTTCGGAATCGTTTTT 3582
DB	911 AAAAGTTGGGCTTCGGAATCGTTTTT 935

RESULT 10

RESULT 10

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8281 973 bp mRNA linear EST 03-JUN-2003  
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 8281  
 8281.1 GI:31373021

erella zeae  
 erella zeae  
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 creomyetidae; Hypocreales; Nectriaceae; Gibberella.  
 bases 1 to 973)  
 on,R.J., Heyes,R., Chapados,J., Couroux,P., Harris,L.J.,  
 ori,J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A.,

TITLE  
 JOURNAL  
 COMMENT

Sprott,D. and Tinker,N.A.  
 A cDNA library prepared from Fusarium graminearum grown  
 complex plant substrate  
 Unpublished (2003)  
 Contact: Watson, Robert.J.  
 Eastern Cereal and Oilseed Research Centre  
 Agriculture and Agri-food Canada  
 Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1  
 CANADA

Tel: (613) 759-1655  
 Fax: (613) 759-1701  
 Email: watsonrj@agr.gc.ca.

Location/Qualifiers

source

1. 973  
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 substrate"

/note="Vector: pBluescript II+; Site 1: EcoRI;  
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 molecular weight, water-soluble components."

ORIGIN

Query Match 14.4%; Score 915.8; DB 14; Length 973;  
 Best Local Similarity 98.6%; Pred. No. 6e-136;  
 Matches 928; Conservative 5; Mismatches 7; Indels 1;

QY 5431 TCATCCATAGTGTGCTGACTCCCGTCTGTGTAGATAACTAGATACGGAGGGC  
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 QY 5971 CCGAGTTGCTCTTGGCGGCGCTCAATACGGGATTAATACGGCGGCACATAGCAGT  
 Db 426 CCGAGTTGCTCTTGGCGGCGCTCAATACGGGATTAATACGGCGGCACATAGCAGT



1124 1089 bp mRNA linear EST 30-JUL-2002  
 1124 Oncorhynchus mykiss Kidney infected by infectious  
 -opoletic necrosis virus Oncorhynchus mykiss cdna clone KG'12,  
 sequence.  
 1124  
 1124.1 GI:6431472  
 rhynchus mykiss (rainbow trout)  
 rhynchus mykiss  
 ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 opterygii; Neopterygii; Teleostei; Euteleostei;  
 acanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 cases 1 to 1089)  
 .T., Sakai,M. and LaPatra,S.B.  
 ssed Sequence Tag Analysis of Kidney and Gill Tissues from  
 ow Trout (Oncorhynchus mykiss) Infected with Infectious  
 opoletic Necrosis Virus  
 Biotechnol. 2 (5), 493-498 (2001)  
 act: Masahiro Sakai  
 lty of Agriculture  
 aki University  
 ishi Gakuenkibandai, Miyazaki, Miyazaki 889-2192, Japan  
 l: m.sakai@cc.miyazaki-u.ac.jp.  
 Location/Qualifiers  
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14.58; Score 926.4; DB 9; Length 1089;  
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 Qy 5097 TACCTTCGGAAGAGTGTGAGTCTT-GATCCGGCAACAAACCA---CCG  
 Db 978 TACCTTCGGAAGAGTGTGAGTCTT-GATCCGGCAACAAACCAACACCGCT  
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RESULT 6  
 AJ281480  
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 VERSION AJ281480.1 GI:6929360  
 KEYWORDS EST.  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Ptery  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea  
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 REFERENCE 1 (bases 1 to 1004)  
 Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Robe  
 Donohue, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., S  
 and Kafatos, F.C.  
 Anopheles gambiae pilot gene discovery project: identifi  
 mosquito innate immunity genes from expressed sequence t  
 generated from immune-competent cell lines  
 Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)  
 20300950  
 MEDLINE 10841561  
 PUBMED  
 COMMENT Contact: Dimopoulos G  
 Fotis C. Kafatos Laboratory  
 European Molecular Biology Laboratory  
 Meyerhofstrasse 1, 69117 Heidelberg, Germany.  
 Location/Qualifiers  
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1137 1067 bp mRNA linear EST 30-JUL-2002  
 1137 Oncorhynchus mykiss Kidney infected by infectious  
 topoietic necrosis virus Oncorhynchus mykiss cDNA clone KI2,  
 sequence.  
 1137  
 1137.1 GI:6431485  
 rhynchus mykiss (rainbow trout)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
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 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhyn  
 1 (bases 1 to 1067)  
 Kono,T., Sakai,M. and LaPatra,S.E.  
 Expressed Sequence Tag Analysis of Kidney and Gill Tissue  
 Rainbow Trout (Oncorhynchus mykiss) Infected with Infect  
 Hematopoietic Necrosis Virus  
 Mar. Biotechnol. 2 (5), 493-498 (2001)  
 Contact: Masahiro Sakai  
 Faculty of Agriculture  
 Miyazaki University  
 1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192,  
 Email: m.sakai@cc.miyazaki-u.ac.jp.

# FEATURES

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## ORIGIN

Query Match 15.0%; Score 954.6; DB 9; Length 1067;  
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 Db 137 ATTCACACACATACGAGCGGGAAGCATAAAGTGTAAAGCTCGGCTGCTAA  
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 Db 197 AGCTAACTCATTAATTTGGTTCGCTCACTGCGCGCTTCCAGTCGGGAAC  
 QY 4378 TGGCAGCTGCAATTAATGAATCGGCAACCGCGGGGAGAGCGGTTTCGCTATT  
 Db 257 TGGCAGCTGCAATTAATGAATCGGCAACCGCGGGGAGAGCGGTTTCGCTATT  
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 Db 317 TCTTCGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG  
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 Db 377 TCAGCTCACTCAAGGCGGTAATACGGTTATCCACAGATCAGGGGATACGCA  
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cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996) : Normalization and Subtraction: Two approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806."

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 VERSION BM438846.1 GI:18460568  
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 SOURCE Ictalurus punctatus (channel catfish)  
 ORGANISM Ictalurus punctatus  
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 Ictaluridae; Ictalurus.  
 REFERENCE 1 (bases 1 to 1013)  
 AUTHORS Feng, J., Kucuktas, H., Kocabas, A., Li, P. and Liu, Z.  
 TITLE Transcriptome of channel catfish (Ictalurus punctatus): analysis of expressed sequence tags from the liver  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Liu ZJ  
 The Fish Molecular Genetics and Biotechnology Laboratory  
 Department of Fisheries and Allied Aquacultures and Program in Cell  
 and Molecular Biosciences  
 Auburn University  
 203 Swingle Hall, Auburn University, Auburn, AL 36849, U.S.A.  
 Tel: 334 844 4054  
 Fax: 334 844 9208  
 Email: zliu@acesag.auburn.edu  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

leic search, using sw model

July 15, 2004, 07:32:41 ; Search time 14541 Seconds  
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13092.043 Million cell updates/sec

US-10-668-496-2

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IDENTITY NUC

3apop 10.0 , Gapext 1.0

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Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_eatov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
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# SUMMARIES

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ACCESSION AJ281552  
VERSION AJ281552.1 GI:6929432  
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Ptery  
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Anopheles.  
REFERENCE 1 (bases 1 to 1070)  
AUTHORS Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Robe  
Donhue, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., S  
and Kafatos, F.C.  
TITLE Anopheles gambiae pilot gene discovery project: identifi  
mosquito innate immunity genes from expressed sequence t  
generated from immune-competent cell lines  
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)  
JOURNAL MEDLINE 20300950  
PUBMED 10841561  
COMMENT Contact: Dimopoulos G  
Fotis C. Kafatos Laboratory  
European Molecular Biology Laboratory  
Meyerohofstrasse 1, 69117 Heidelberg, Germany.

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 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Plasmid  
 US-10-395-894-12

Query Match 56.1%; Score 3578.4; DB 13; Length 6097  
 Best Local Similarity 88.9%; Pred. No. 0;  
 Matches 4141; Conservative 0; Mismatches 16; Indels 503;

QY 1750 GAGCTCCAGCTTTTCTGAGCGGAAAGAACAGCTGGGGCTCTAGGGGGTATCC 1804  
 Db 1907 GGGCTCTATGGCTTTCTGAGCGGAAAGAACAGCTGGGGCTCTAGGGGGTATCC 1966  
 QY 1810 GCCCTGTAGCGCGCATTAAGCGCGGGGTGTGTTGTACGCGCAGCGTGAC 1864  
 Db 1967 GCCCTGTAGCGCGCATTAAGCGCGGGGTGTGTTGTACGCGCAGCGTGAC 2024  
 QY 1870 ACTTGCAGCGCCCTAGCGCGCTCTCTTTCGCTTCTTCCCTTCTTCTCGCG 1928  
 Db 2027 ACTTGCAGCGCCCTAGCGCGCTCTCTTTCGCTTCTTCCCTTCTTCTCGCG 2086  
 QY 1930 GCGCGCTTCCCGCTCAAGCTCTAAATCGGGC-TCCTTTTAGGGTTCGATTT 1988  
 Db 2087 GCGCGCTTCCCGCTCAAGCTCTAAATCGGGC-TCCTTTTAGGGTTCGATTT 2146  
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 Db 2147 TTTACGCGCCTCGACCCCAAAAACCTTGTAGGGGTGATGGTTTACGTAGTGC 2206  
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QY 4056 TATTGACGCTTATAATGGTTTCAAAATAAGCAATAGCATCAAAATTTCAAAA  
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## RESULT 12

US-10-395-894-11  
; Sequence 11, Application US/10395894  
; Publication No. US20040033229A1  
; GENERAL INFORMATION:  
; APPLICANT: MADDON, Paul J.  
; APPLICANT: DOROVAN, Gerald P.  
; APPLICANT: OLSON, William C.  
; APPLICANT: SCHLICK, No. US20040033229A1  
; APPLICANT: GARDNER, Jason  
; APPLICANT: MA, Dangshe  
; TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS  
; FILE REFERENCE: P00741.70005 US  
; CURRENT APPLICATION NUMBER: US/10/395,894  
; CURRENT FILING DATE: 2003-03-24  
; PRIOR APPLICATION NUMBER: PCT/US02/33944  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: US 60/335,215  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 60/362,747  
; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: US 60/412,618  
; PRIOR FILING DATE: 2002-09-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
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; TYPE: DNA

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Dc	262	CTCCGCCCATGGCTGACTAAATTTTATTTATGTCAGAGGCCGAGGCGCTCTGCC	2663
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Dc	332	CACGGCGAGGATCTCGTCGTGAACCATGGCGCATGCTGCTTGCAGATATCATGGTGGAA	3383
Qy	327	AATGGCCGCTTTTCGTGATTCATCGACTGTGGCCGGCTGGGTGGCGGACCGCTATCAG	3335
Dc	338	AATGGCCGCTTTTCGTGATTCATCGACTGTGGCCGGCTGGGTGGCGGACCGCTATCAG	3443
Qy	333	GACATAGCTTGGCTACCCGTGATATGCTGAGAGGCTTGGCGGCGAATGGGCTGACCGC	3395
Dc	344	GACATAGCTTGGCTACCCGTGATATGCTGAGAGGCTTGGCGGCGAATGGGCTGACCGC	3503
Qy	339	TTCTCTGTGCTTTAACGTATCGCCGCTCCCGAATTCGACGCGCATCGCCTTCTATCGCTT	3455
Dc	350	TTCTCTGTGCTTTAACGTATCGCCGCTCCCGAATTCGACGCGCATCGCCTTCTATCGCTT	3563
Qy	345	CTTGAACGAGTCTTCTGAGCGGGAACCTCGGGGTTTCGAAATGACCGCAAGCAGCGCCA	3515
Dc	356	CTTGAACGAGTCTTCTGAGCGGGAACCTCGGGGTTTCGAAATGACCGCAAGCAGCGCCA	3623
Qy	351	ATCTGCCCATCAGGATTTGATTTCCACCGCGGCTTCTATGAAAGGTTGGGCTTCGGA	3575

Db	3624	ACCTGCCATC-----	3633
QY	3576	TCGTTTTCGCGACGCCGGCTGGATGATCCTCCAGCGCGGGATCTCATGCTGG	3625
Db	3634	-----	3623
QY	3636	TCGCCACCTTAGGGGAGGCTAACTGAACAACGGAGGAGACAATACCGGAAG	3695
Db	3634	-----	3633
QY	3696	CGCATGACGGCAATAAAGACAGAAATAAAGCGACGGTGTGGGTGCTTTGT	3759
Db	3634	-----	3633
QY	3756	ACGGGGTTCGGTCCCGAGGCTGGCACTCTGTGATACCCACCGAGACCCCA	3815
Db	3634	-----	3633
QY	3816	CCAATACCGCGGTTCCTCTCTTTCCCAACCCACCCCCCAAGTTCGGGTGA	3873
Db	3634	-----	3633
QY	3876	AGGCTCGACGCCAACGTGCGGGGGCAGGCCCTCGCATAGCTCAGTGTCTACG	3935
Db	3634	-----ACG-----	3642
QY	3936	CGATTCCACCGCGCCTTCTATGAAGGTTGGGCTTCGGAACTCGTTTTCGGGA	3995
Db	3643	CGATTCCACCGCGCCTTCTATGAAGGTTGGGCTTCGGAACTCGTTTTCGGGA	3995
QY	3996	CTGGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTCTTCGCCCAACCCCAA	4055
Db	3703	CTGGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTCTTCGCCCAACCCCAA	4055
QY	4056	TATTGCAGCTTAAATGGTTACAAATAAGCAATAGCATCACAAATTCACAAA	4115
Db	3763	TATTGCAGCTTAAATGGTTACAAATAAGCAATAGCATCACAAATTCACAAA	4115
QY	4116	ATTTTTTTCACCTGATTTAGTTGTGGTTGTCCAAACTCATCAATGTATCTTTA	4175
Db	3823	ATTTTTTTCACCTGATTTAGTTGTGGTTGTCCAAACTCATCAATGTATCTTTA	4175
QY	4176	CTGTATACCGTGCACCTCTAGCTAGAGCTTGGCGTAATCATGGTCTATAGCTGT	4235
Db	3883	CTGTATACCGTGCACCTCTAGCTAGAGCTTGGCGTAATCATGGTCTATAGCTGT	4235
QY	4236	GTGAATTTGTTATCCGCTCACAATTCACACACATACGAGCGCGAAGCATAA	4295
Db	3943	GTGAATTTGTTATCCGCTCACAATTCACACACATACGAGCGCGAAGCATAA	4295
QY	4296	AGCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGGTTGGGTCACTG	4355
Db	4003	AGCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGGTTGGGTCACTG	4355
QY	4356	TTTCCAGTCCGGAAACCTGTGTCGCCAGCTGCATTAAATGAATCGGCCAACGGCG	4415
Db	4063	TTTCCAGTCCGGAAACCTGTGTCGCCAGCTGCATTAAATGAATCGGCCAACGGCG	4415
QY	4416	AGCGGTTTTCGTATTGGGGGCTCTTCGGGTTCTCGCTCACTGACTCGCTGCG	4475
Db	4123	AGCGGTTTTCGTATTGGGGGCTCTTCGGGTTCTCGCTCACTGACTCGCTGCG	4475
QY	4476	CGTTTCGGTTCGCGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGGTTATCC	4535
Db	4183	CGTTTCGGTTCGCGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGGTTATCC	4535
QY	4536	ATCAGGGGATTAACGACAGGAAAGAACTGTGAGCAAAAGCCACGAAAAGGCCAGK	4595
Db	4243	ATCAGGGGATTAACGACAGGAAAGAACTGTGAGCAAAAGCCACGAAAAGGCCAGK	4595
QY	4596	TAAAAAGGCGGTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTCTGACGAGCA	4655
Db	4303	TAAAAAGGCGGTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTCTGACGAGCA	4655



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; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 6082  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid  
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Query Match 56.1%; Score 3578.4; DB 13; Length 6082  
Best Local Similarity 88.9%; Pred. No. 0;  
Matches 4141; Conservative 0; Mismatches 16; Indels 503;  
  
QY 1750 GAGCTCCAGCTTTTCTGAGCGCGAAAGAACAGCTGGGGCTCTAGGGGGTATCC  
DB 1892 GGGCTCTATGGCTTCTGAGCGCGAAAGAACAGCTGGGGCTCTAGGGGGTATCC  
QY 1810 GCCCTGTAGCGCGCATTAAGCGCGCGGGTGTGGTGTACGGCGACGGTAC  
DB 1952 GCCCTGTAGCGCGCATTAAGCGCGCGGGTGTGGTGTACGGCGACGGTAC  
QY 1870 ACTTGGCCAGCGCCCTAGCGCGCGCTCTTTCGCTTCTTTCCTTCTTCTTCGC  
DB 2012 ACTTGGCCAGCGCCCTAGCGCGCGCTCTTTCGCTTCTTTCCTTCTTCTTCGC  
QY 1930 CGCGGGCTTCCCGCTCAAGCTCTAAATCGGGGCTCTTTCGCTTCTTTCCTTTCGC  
DB 2072 CGCGGGCTTCCCGCTCAAGCTCTAAATCGGGGCTCTTTCGCTTCTTTCCTTTCGC  
QY 1989 TTTACGGCAGCTCGACCCCAAAAACTTGTATAGGGTGTGGTTCACGTAGTGG  
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QY 2049 GCCCTGTAGTAGCGGTTTTTCGCTTCTTTCGCTTCTTTCCTTCTTCTTCGC  
DB 2192 GCCCTGTAGTAGCGGTTTTTCGCTTCTTTCGCTTCTTTCCTTCTTCTTCGC  
QY 2109 CTGTGTTCCAAACTGGAACAACAACCTATCTCGGTCTATTTCTTTTGAATTT  
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DB 2424 CCCCAGGAGGAGGATATGCAAGGATGATCTCAATTTAGTCTAGGCAACGAGC  
QY 2408 AAGTCCCCAGGCTCCCCAGGAGGAGGATATGCAAGGATGATCTCAATTTAG  
DB 2484 AAGTCCCCAGGCTCCCCAGGAGGAGGATATGCAAGGATGATCTCAATTTAG  
QY 2468 ACCATAGTCTCCGCGCCCTTAACTCCGCGCCATCCGCGCCCTTAACTCCGCGCCAGTTTC

QY 1336 G C A T A G C G T T G G C T A C C C G T G A T A T T G C T G A A G A G C T T T G G G G G A A T G G C T G A C C G C 3395  
 Db 1444 G C A T A G C G T T G G C T A C C C G T G A T A T T G C T G A A G A G C T T T G G G G G A A T G G C T G A C C G C 3503  
 QY 1396 T T C C T C G T G C T T A G G T A T C C G C G T C C G G T T C C G A T T C G C A G C G A T C G C C T T C T A T G C C T T 3455  
 Db 1504 T T C C T C G T G C T T A G G T A T C C G C G T C C G G T T C C G A T T C G C A G C G A T C G C C T T C T A T G C C T T 3563  
 QY 1456 C T T G A C G A G T T C T T C T G A C G G G A C T C T G G G G T T C G A A T G A C C G A C C A A G C G A G C C C A 3515  
 Db 1564 C T T G A C G A G T T C T T C T G A C G G G A C T C T G G G G T T C G A A T G A C C G A C C A A G C G A G C C C A 3623  
 QY 1516 A C C T G C G A T C A C G A G A T T C G A T T C C A C G C G C C T T C T A T G A A A G G T T G G G C T T C G G A A 3575  
 Db 1624 A C C T G C C A T C ----- 3633  
 QY 1576 T T G T T T C C G G A C G C G G C T G G A T A T C T C C A G C G G G G A T C T A T G C T G G A G T T C T 3635  
 Db 1634 ----- 3633  
 QY 1636 T T G C C C A C C T A G G G G G A G G C T A A C T G A A C A C G G A A G G A G A C A A T A C C G A A G G A A C C C 3695  
 Db 1634 ----- 3633  
 QY 1696 G C A T G A C G G C A T A A A A G A C A G A T A A A C G C A C G G T T G G G T C G T T T G T T C A T A A 3755  
 Db 1634 ----- 3633  
 QY 1756 A G C G G G G T T C G G T C C C A G G G T G G C A C T C T G T G A T A C C C A C C A G A C C C A T T G G G 3815  
 Db 1634 ----- 3633  
 QY 1816 C A A T A C G C C C G G T T C T T C T T T T C C C A C C C A C C C C A A G T T C G G T G A A G G C C 3875  
 Db 1634 ----- 3633  
 QY 1876 A T G G C T C G C A C C A A G T C G G G G C G C A G C C C T G C C A T A G C C T A G C T C A G T C T A C G A G A T T T 3935  
 Db 1634 ----- A C G A G A T T 3642  
 QY 936 C G A T T C C A C G C G C C T C T A T A A A G T T G G G C T T C G S A A T C G T T T C G G G A C G C C G G 3995  
 Db 1643 C G A T T C C A C G C G C C T C T A T A A A G T T G G G C T T C G S A A T C G T T T C G G G A C G C C G G 3702  
 QY 996 C T G A A T A P C C T C C A G C G C G G A T C T A T G C T G G A G T T C T T C G C C C A C C C C A A C T T G T T 4055  
 Db 703 C T G A T G A T C C T C C A G C G C G G A T C T A T G C T G G A G T T C T T C G C C C A C C C C A A C T T G T T 3762  
 QY 1056 T A T T C G A G C T T A T A T G G T T A C A A A T A A G C A A T A G C A T C A C A A T T T C A C A A A T A A A G C 4115  
 Db 763 T A T T C G A G C T T A T A T G G T T A C A A A T A A A G C A A T A G C A T C A C A A T T T C A C A A A T A A A G C 3822  
 QY 1116 A T T T T T T C A C T G C A T T C T A G T T G T G T T G T T C C A A A C T C A T A A T G T A T C T T A T C A T G T 4175  
 Db 1823 A T T T T T T C A C T G C A T T C T A G T T G T G T T G T T C C A A C T C A T C A A T G T A T C T T A T C A T G T 3882  
 QY 1276 C T G T A T A C G T C G A C C T C T A G C T A G A G T T G C G T A A T C A T G G T C A T A G C T G T T T C C T G T 4235  
 Db 1883 C T G T A T A C G T C G A C C T C T A G C T A G A G T T G C G T A A T C A T G T C A T A G C T G T T T C C T G T 3942  
 QY 1236 G T G A A T T G T A T C G C T C A C A A T T C C A C A A C A T A C A G A C C G A A G A C A T A A A G T G T A A 4295  
 Db 1943 G T G A A T T G T A T C G C T C A C A A T T C C A C A A C A T A C A G A C C G A A G A C A T A A A G T G T A A 4002  
 QY 1296 A T C C T G G G G T G C T A A T A G T G A G C T A A C T C A C A T T A A T T G G T T G C G C T C A C T C C C C G C 4355  
 Db 1003 A T C C T G G G G T G C T A A T A G T G A G C T A A C T C A C A T T A A T T G G T T G C G C T C A C T C C C C G C 4062  
 QY 1356 T T C A G T C G G A A A C C T G T C G T C C A G C T G C A T T A A T G A A T C G G C C A A C G C G C G G G A G 4415  
 Db 1063 T T C C A G T C G G A A A C C T G T C G T C C A G C T G C A T T A A T G A A T C G G C C A A C G C G C G G A G 4122

QY 4416 A G C G G T T T G G C T A T T G G G C G C T C T T C G C G T T C C T C G C T C A C T G A C T C G C T G C G 4475  
 Db 4123 A G C G G T T T G G C T A T T G G G C G C T C T T C G C T C C T C G C T C A C T G A C T C G C T G C G 4182  
 QY 4476 C G T T C G C T G C G C G A G C G G T A T C A G C T A C T C A A A G C G G T A A T A C G G T T A T C 4535  
 Db 4183 C G T T C G C T G C G C G A G C G G T A T C A G C T C A C T C A A A G C G G T A A T A C G G T T A T C 4242  
 QY 4536 A T C A G G G A T A A C G C A G A A A G A C A T C T G A G C A A A A G C C A G A A A A A G C C A G 4595  
 Db 4243 A T C A G G G A T A A C G C A G A A A G A C A T C T G A G A A A A G C C A G A A A A A G C C A G 4302  
 QY 4596 T A A A A G C C C G T T G C T G G G C T T T T T C A T A G G C T C G C C C C C C C T G A C G A C A 4655  
 Db 4303 T A A A A G C C G T T G C T G G G C T T T T T C A T A G G C T C G C C C C C C C T G A C G A C A 4362  
 QY 4656 A A A T C G A C G C T C A G T C A G A G G T G C G A A C C C A C A G A C C A C T A T A A A G A T A C C A 4715  
 Db 4363 A A A T C G A C G C T C A G T C A G A G G T G C G A A C C C A C A G A C C A C T A T A A A G A T A C C A 4422  
 QY 4716 T C C C C T C G A A G C T C C C T C G T G C G C T C C T G T T C C G A C C C T G C G C T T A C C G G 4773  
 Db 4423 T C C C C T C G A A G C T C C C T C G T G C G C T C C T G T T C C G A C C C T G C G C T T A C C G G 4482  
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 Db 4483 G T C G C C T T T C C C T T C G G A A G C G T G G C G C T T T C A A T G C T C A C G C T G T A G 4542  
 QY 4836 C A G T T C G G T G T A G T T C G C T C C A G C T G G C T G T G T G C A C G A C C C C C G T 4895  
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 Db 4663 A T C G C C A C T G G A G C A G C C A C T G G T A A C A G G A T T A G A G A G C G A G G T A T G T A G G 4723  
 QY 5016 T A C A G A G T T C T G A A G T G G T G C C C T A C T A G C G T A C A C T A G A A G A C A G A T T T 5075  
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 QY 5256 A A A C T C A C G T T A A G S G A T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T 5315  
 Db 4963 A A A C T C A C G T T A A G S G A T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T 5023  
 QY 5316 T T T A A A T T A A A A T G A A G T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T T 5375  
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 QY 5376 C A G T T T A C C A A T G C T T A A T C A G T A G G C A C C T A T C T C A G C G A T C T G T C T A T T T C G 5435  
 Db 5083 C A G T T A C C A A T G C T T A A T C A G T A G G C A C C T A T C T C A G C G A T C T G T C T A T T T C G 5142  
 QY 5436 C A T A G T T G C C T G A C T C C C C G T C G T G T A G A T A A C T A C G A T A C G G A G G C G C T T A C C 5495  
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 QY 5496 C C C A G T G C T C A A T G A T A C C G C G A G A C C C A C G C T C A C C G C T C C A G A T T T A T C 5555



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Db	4963	AAACTCAGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTTA	53017	53021
Qy	5316	TTTAAATTTAAATATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGG	53254	53258
Db	5023	TTTAAATTTAAATATGAAGTTTAAATCAGTCTAAAGTATATATGAGTAAACTTGG	53274	53282
Qy	5376	CAGTTACCAATGCTTAATCAGTAGGAGCACCTATCTCAGCGCATCTGTCTATTTCG	53435	53439
Db	5083	CAGTTACCAATGCTTAATCAGTAGGAGCACCTATCTCAGCGCATCTGTCTATTTCG	53470	53482
Qy	5436	CATAGTTGCTGACTCCCGCTCGTGTAGATAAATACTACGATACGGAGGGCTTACC	53595	53599
Db	5143	CATAGTTGCTGACTCCCGCTCGTGTAGATAAATACTACGATACGGAGGGCTTACC	53610	53622
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Qy	5616	CCAGTCTATTAAATTTGTTCCGGGAAGCTACAGTAAGTAGTTCGCCAGTTAATAG	53750	53754
Db	5323	CCAGTCTATTAAATTTGTTCCGGGAAGCTACAGTAAGTAGTTCGCCAGTTAATAG	53757	53769
Qy	5676	CAACGTTGTTGCCATTTGCTACAGGCATCGTGGTGTCAACGCTCGTCTGTTTCGGTAT	53790	53794
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Qy	5736	ATTTCAGCTCCGGTTCOCAACGATCAAGGGCAGTTACATGATCCCCCATGTGTGG	53844	53856
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Qy	5796	AGCGGTTAGTCTCTTCCGTCTCCGATCGTGTGTACAGATGAAGTTGGCCCGCAGT	53902	53914
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Db	5623	TTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTCAGAAATAGTGTATCGCGCG	54050	54062
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RESULT 9
US-10-395-894-8
; Sequence 8, Application US/10395894
; Publication No. US20040033229A1
; GENERAL INFORMATION:
; APPLICANT: MADDON, Paul J.
; APPLICANT: DONOVAN, Gerald P.
; APPLICANT: OLSON, William C.
; APPLICANT: SCHSLKE, No. US20040033229A1bert
; APPLICANT: GARDNER, Jason
; APPLICANT: MA, Dangshe
; TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS
; FILE REFERENCE: P00741.70005.US
; CURRENT APPLICATION NUMBER: US/10/395,894
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: PCT/US02/33944
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/335,215
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/362,747
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/412,618
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid
; US-10-395-894-8

Query Match 56.1%; Score 3578.4; DB 13; Length 6082
Best Local Similarity 88.9%; Pred. No. 0;
Matches 4141; Conservative 0; Mismatches 16; Indels 503;

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DE 1952 GCCCTGTAGCGCGCATTAAGCGGCGGGGTGTGGTGTACGCGCAGCGTAC 1901
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## RESULT 7

US-09-559-874-5  
; Sequence 5, Application US/09559874  
; Publication No. US20020192726A1

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; Sequence 3, Application US/09844645
; Patent No. US20020102242A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
;             Curiel, David T.
;             McDaniel, Larry E.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
;                     ADMINISTERING PNEUMOCOCCAL DNA
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/844,645
; FILING DATE: 27-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/759,505
; FILING DATE: 04-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5446 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-844-645-3

Query Match          56.1%; Score 3578.4; DB 9; Length 5446;
Best Local Similarity 88.9%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 16; Indels 503;

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E: 514429-3785
CATION NUMBER: US/09/794,975
G DATE: 2001-02-27
TION NUMBER: US 09/455,367
DATE: 1999-12-03
TION NUMBER: 19856261.6
DATE: 1998-12-07
, ID NOS: 13
entIn Ver. 2.1

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Official Sequence

ATION: Description of Artificial Sequence: mutagen

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Conservative	0; Mismatches 16; Indels 503; Gaps 5;	
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## RESULT 4

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US-10-115-440-8
; Sequence 8, Application US/10115440
; Publication No. US20040086845A1
; GENERAL INFORMATION:
; APPLICANT: WU, Tzyy-Choo
; APPLICANT: HUNG, Chien-Fu
; TITLE OF INVENTION: SUPERIOR MOLECULAR VACCINE LINKING THE TRANSLATION DOMAIN OF A
; TITLE OF INVENTION: BACTERIAL TOXIN TO AN ANTIGEN
; FILE REFERENCE: 02240-179934
; CURRENT APPLICATION NUMBER: US/10/115,440
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 60/281,003
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: PCT/US00/41422
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 09/501,097
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/421,608
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
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US-10-115-440-8
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Query Match 56.1%; Score 3578.4; DB 17; Length 5431
Best Local Similarity 88.9%; Pred. No. 0;
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us-10-668-496-2.rnpb

GenCore version 5.1.6  
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JS-10-668-496-2

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IDENTITY\_NUC

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angth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
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- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

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ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

#### SUMMARIES

Query Match	Length	DB	ID	Description
56.2	6431	16	US-10-340-447-4	Sequence 4, Appli
56.2	7427	17	US-10-617-619-13	Sequence 13, Appl
56.2	7493	17	US-10-617-619-10	Sequence 10, Appl
56.1	5431	17	US-10-115-440-8	Sequence 8, Appli
56.1	5432	9	US-09-794-975-9	Sequence 9, Appli
56.1	5446	9	US-09-844-645-3	Sequence 3, Appli
56.1	5446	9	US-09-559-874-5	Sequence 5, Appli
56.1	5446	16	US-10-371-116A-1	Sequence 1, Appli
56.1	6082	13	US-10-395-894-8	Sequence 8, Appli
56.1	6082	13	US-10-395-894-9	Sequence 9, Appli
56.1	6082	13	US-10-395-894-10	Sequence 10, Appli
56.1	6085	13	US-10-395-894-11	Sequence 11, Appli
56.1	6094	13	US-10-395-894-13	Sequence 13, Appli
56.1	6097	13	US-10-395-894-12	Sequence 12, Appli

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16	3578.4	56.1	6221	17	US-10-115-440-9	Sequenc
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#### ALIGNMENTS

RESULT 1  
US-10-340-447-4  
; Sequence 4, Application US/10340447  
; Publication No. US20040002115A1  
; GENERAL INFORMATION:  
; APPLICANT: FRAISSIGNES, Pauline  
; APPLICANT: GRATZER, Sabine  
; APPLICANT: LEBERER, Ekkehard  
; TITLE OF INVENTION: METHOD OF IDENTIFYING PROTEIN CAMS (CONSTITUT  
; TITLE OF INVENTION: MUTANTS)  
; FILE REFERENCE: DEAV2002/0003 USNP  
; CURRENT APPLICATION NUMBER: US/10340,447  
; PRIOR FILING DATE: 2003-01-10  
; PRIOR APPLICATION NUMBER: DE 02000733.2  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 6431  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Nucleotide Sequence of pcDNA3.1(+) - Edge 5  
US-10-340-447-4

Query Match	56.2%	Score	3581.4	DB	16	Length	6431
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Db	2305	GCCTGTAGCGGCGCATTTAGCGCGGGGTGTGTGTTACGCGCAGCGTGAC					



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Db 3687 GTGAAATTTGTTATTCGGCTCAAAATTCACACAAACATACGAGCGGAGCATAAA  
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Qy 4536 ATCAGGGGATACCGAGGAAAGACATGTGAGCAAAAGGCGCAGCAAAAGGCGAG  
Db 3987 ATCAGGGGATACCGAGGAAAGACATGTGAGCAAAAGGCGCAGCAAAAGGCGAG  
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Db 4107 AAATCGACGCTCAAGTCAAGGTTGGCGAAACCCGACAGGACTATAAAGATACCA  
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Db 4167 TCCCCCTGGAGGCTCCCTCGGCTCTCTCTGTTTCGACCTCGGCTTACCGG  
Qy 4776 GTCCGCTTCTTCTCGGGAAGCGGCGCTTCTCATAGCTCACCGCTGAG  
Db 4227 GTCCGCTTCTTCTCGGGAAGCGGCGCTTCTCATAGCTCACCGCTGAG  
Qy 4836 CAGTTCCGTTAGGTCGTTTCCTCAAGCTCGGCTGTGTGACGAAACCCCGGCT  
|||||





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CTGGAGTCTTCGCCCAACCCCAACTTGTGTTTATGAGCTTATAATGTTTACAAATAAA 3366  
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Db 4563 GATTATCAAAAAGGATCTTCACTAGATCCTTTTAAATTAATAATGAAGTTTAA  
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Db 4623 TCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTG  
QY 5405 CTATCTCAGCGATCTGTCTATTTTCGTTTCACTCATAGTTGCTGATCCTCCGCTG  
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QY 5525 CACGCTCACCGGCTCCAGATTATCAGCAATAAAGCAGCCAGCCGCGAAGGCGCG  
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 DE 1668 GAGCTGTAGAGCGTTTTCGCGCTTTGAGTTCAGCTTCTTTAATAGTGGACT 1727  
 QY 2109 CTGTGTTCCAACTGGAAACAACTCAACCTATCTCGGTCTATTTCTTTGATTTAAGG 2168  
 DE 1726 CTGTGTTCCAACTGGAAACAACTCAACCTATCTCGGTCTATTTCTTTGATTTAAGG 1787  
 QY 2169 GATTTTGGCGATTTTCGCGCTATTTGTTTAAAAATGAGCTGATTTAAACAAAAATTTAAAGC 2228  
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 DB 1968 TGTCAAGTTAGGGTGTGGAAGTCCCGAGCTCCCGAGCAGCAGCAAGTATGCAAGCAT 2027  
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ACCAGCCAGCGGAAGGCGCGAGCGCAGAAGTGTCTCTCAACTTTATCCGCTCCAT 15429

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Db	15850	GCTCATCA TTGGAAGCGTTCTTCGGGGCGAAAAC TCTCAAGGATCTTACCGCTCT
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Qy	6336	GGTTCCGCGACATTTCCCCGAAAAGTGCACTGACGTC 6375
Db	16150	GGTTCCGCGACATTTCCCCGAAAAGTGCCACTGACGTC 16189

## RESULT 14

US-08-073-836-3  
Sequence 3, Application US/08073836  
Patent No. 5650306  
GENERAL INFORMATION:  
APPLICANT: Nabel, Gary J.  
APPLICANT: Yang, Zhi-yong  
APPLICANT: Liu, Jin-song  
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACIDS FOR INHIBITING  
TITLE OF INVENTION: HIV GENE EXPRESSION  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073,836  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UM 9646  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5653 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-073-836-3

Query Match 56.1%; Score 3577; DB 1; Length 5653;  
Best Local Similarity 88.6%; Pred. No. 0;  
Matches 4156; Conservative 0; Mismatches 65; Indels 470;



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|||||

plication US/09236140A

6236

SMATION:

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Polo, John M.  
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Chang, Stephen M.W.  
Jolly, Douglas J.  
Driver, David A.  
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F INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES

OF SEQUENCES: 124

DENSE ADDRESS:

DRESSEE: OPPENHEIMER WOLFF & DONNELLY

REET: 840 NEWPORT CENTER DRIVE, SUITE 700

TY: NEWPORT BEACH

ATE: CALIFORNIA

JNTRY: US

P: 92660

3 READABLE FORM:

DIUM TYPE: Floppy disk

MPUTER: IBM PC compatible

ERATING SYSTEM: PC-DOS/MS-DOS

FTWARE: Patent In Release #1.0, Version #1.25

APPLICATION DATA:

PLICATION NUMBER: US/09/236,140A

LING DATE: 22-Jan-1999

ASSIFICATION: <Unknown>

Y/AGENT INFORMATION:

ME: Cullman, Louis C.

ISTRATION NUMBER: 39,645

REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020

FOR SEQ ID NO: 1:

LEPHONE: (949) 823.6000

LEFAX: (949) 823.6100

E CHARACTERISTICS:

NGTH: 16656 base pairs

PE: nucleic acid

RANDEDNESS: single

POLOGY: linear

E DESCRIPTION: SEQ ID NO: 1:

US-09-236-140A-1

Query Match 56.18; Score 3578.4; DB 4; Length 16656  
Best Local Similarity 88.94; Pred. No. 0;  
Matches 4141; Conservative 0; Mismatches 16; Indels 503;

Qy	1750	GAGCTCTCAGCGCTTTTCTGAGCGCGGAAAGAACCCAGCTGGGGCTCTAGGGGGGTATCC	
Db	11999	GGGCTCTATGGCTTCTGAGCGCGGAAAGAACCCAGCTGGGGCTCTAGGGGGGTATCC	
Qy	1810	GCCTGTGAGCGCGCATTAAGCGCGCGGGTGTGGTTAAGCGCGAGCGTGAC	
Db	12059	GCCTGTGAGCGCGCATTAAGCGCGCGGGTGTGGTTAAGCGCGAGCGTGAC	
Qy	1870	ACTTGCAGCGCCTAGCGCGCGCTTTCGCTTTCGCTTTCCTTCCCTTCTTCGCG	
Db	12119	ACTTGCAGCGCCTAGCGCGCGCTTTCGCTTTCGCTTTCCTTCCCTTCTTCGCG	
Qy	1930	CGCGCGCTTTCCTCGTCAAGCTCTAAATCGGGG-TCCTTTTAAAGGTTCCGATT	
Db	12179	CGCGCGCTTTCCTCGTCAAGCTCTAAATCGGGGATCCCTTAAAGGTTCCGATT	
Qy	1989	TTTACGCGACCTCGACCCCAAAAACTTGATTTAGGGTGATGTTCAAGTAGTG	
Db	12239	TTTACGCGACCTCGACCCCAAAAACTTGATTTAGGGTGATGTTCAAGTAGTG	
Qy	2049	GCCTGATAGACGGTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTTAATAG	
Db	12299	GCCTGATAGACGGTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTTAATAG	
Qy	2109	CTTGTTCCAAACCTGGAACCAACACTCAACCTTATCTCGGTCTATTCTTTGATTT	
Db	12359	CTTGTTCCAAACCTGGAACCAACACTCAACCTTATCTCGGTCTATTCTTTGATTT	
Qy	2169	GATTTGCCGATTTTCGCCCTTATGGTTAAAAAATGAGCTGATTTAAACAAAAATT	
Db	12419	GATTTGCCGATTTTCGCCCTTATGGTTAAAAAATGAGCTGATTTAAACAAAAATT	
Qy	2229	GATTTAATCTGTGGAATGCCCGGAGCTTGTATATCCATTTTCGGATCTGATC	
Db	12479	GATTTAAT-----	
Qy	2289	GAGCGGAAAGAACACAGCTGTGGAATGTGTCTAGTTAGGGTGTGAAAGTCCC	
Db	12488	-----CTGTGGAATGTGTCTAGTTAGGGTGTGAAAGTCCC	
Qy	2349	CCCCA-GCAGCGAGAGTATGCAAGCATGCAATCTCAATTAGTCAGCAACAGG	
Db	12531	CCCCAGCGAGCGAGAGTATGCAAGCATGCAATCTCAATTAGTCAGCAACAGG	
Qy	2408	AAGTCCCAGGCTCCCAGCGAGGAGAGTATGCAAGCATGCAATCTCAATTAG	
Db	12591	AAGTCCCAGGCTCCCAGCGAGGAGAGTATGCAAGCATGCAATCTCAATTAG	
Qy	2468	ACCATAGTCCCGCCCTAACTCCGCCCATCCGCCCTTAACTCCGCCCAGTTCC	
Db	12651	ACCATAGTCCCGCCCTAACTCCGCCCATCCGCCCTTAACTCCGCCCAGTTCC	
Qy	2528	TCTCCGCCCATGGCTGACTAAATTTTTTTTTTTTATTTATGAGGCGCGAGCGCC	
Db	12711	TCTCCGCCCATGGCTGACTAAATTTTTTTTTTTTATTTATGAGGCGCGAGCGCC	
Qy	2588	TCTGAGCTATTCCAGAAAGTGTGAGGAGGCTTTTTTGGAGGCTTAGGCTTTTGC	
Db	12771	TCTGAGCTATTCCAGAAAGTGTGAGGAGGCTTTTTTGGAGGCTTAGGCTTTTGC	
Qy	2648	C-----CATCAAGAGACAGGATGAGGA	
Db	12831	CTCCCGGAGCTTGTATATCCATTTTCGGATCTGATCAAGAGACAGGATGAGGA	
Qy	2676	CGCATGATTGACAGAGATGGAATTCACGAGGTTCTCGCGCGCTTGGGTGGAG	
Db	12891	CGCATGATTGACAGAGATGGAATTCACGAGGTTCTCGCGCGCTTGGGTGGAG	

D2 13740 ----- 13740  
QY 13816 C...AATACGCCCGGTTTCTTCTCTTTCCCCACCCACCCCGCAAGTTGGGTGAAGCCC 3875  
D2 13741 ----- 13740  
QY 13874 A...GGCTCGAGCCAAAGTCGGGGCGGACGGCCCTGCGCATAGCCTCAGTGCTACGAGATTT 3935  
D2 13741 -----ACGAGATTT 13749  
QY 13936 C...ATTCCACCGCGCTTCTATGAAGGTTGGCTTCGGAAATCGTTTTCGGGACGCCGG 3995  
D2 13750 C...ATTCCACCGCGCTTCTATGAAGGTTGGCTTCGGAAATCGTTTTCGGGACGCCGG 13809  
QY 1396 C...GGATGATCTCCAGCGCGGGATCTCATGTGGAGTTCTTCGGCCACCCCAACTTGT 4055  
D2 13816 C...GGATGATCTCCAGCGCGGGATCTCATGTGGAGTTCTTCGGCCACCCCAACTTGT 13869  
QY 1056 C...TTGCGAGCTTAAATGGTTACAAATAAAGCAATAGCATCAAAATTTTCAAAATAAAGC 4115  
D2 13870 T...TTGCGAGCTTAAATGGTTACAAATAAAGCAATAGCATCAAAATTTTCAAAATAAAGC 13929  
QY 1114 A...TTTTTTTCACTGCAATCTAGTTTGGTTTGTCCAACTCATCAATGTATCTTATCATGT 4175  
D2 13934 A...TTTTTTTCACTGCAATCTAGTTTGGTTTGTCCAACTCATCAATGTATCTTATCATGT 13989  
QY 1178 C...GTATACCGTCTAGCTAGAGCTTGGCGTAATCATGGTCAATAGCTGTTTCCCTGT 4235  
D2 13901 C...GTATACCGTCTAGCTAGAGCTTGGCGTAATCATGGTCAATAGCTGTTTCCCTGT 14049  
QY 1234 G...GAATTTGTTATCGCTCAATTTCCACAAATACGAGCGGAGCATAAAGTGTA 4295  
D2 1050 G...GAATTTGTTATCGCTCAATTTCCACAAATACGAGCGGAGCATAAAGTGTA 14109  
QY 1296 A...CCTGGGCTGCTAATGAGTGAGCTAACTCAATTTAATGGAATCGCGCGGGAG 4355  
D2 1110 A...CCTGGGCTGCTAATGAGTGAGCTAACTCAATTTAATGGAATCGCGCGGGAG 14169  
QY 1356 T...TCAGTCGGGAAACCTGTCTGTGCGAGCTGATTAATGAATCGCGCGGGAG 4415  
D2 1170 T...TCAGTCGGGAAACCTGTCTGTGCGAGCTGATTAATGAATCGCGCGGGAG 14229  
QY 1416 A...GGCGGTTTGGCTATTTGGCGCTCTTCGGCTTCCTCGCTCACTGACTGCTGCGCTCGT 4475  
D2 1230 A...GGCGGTTTGGCTATTTGGCGCTCTTCGGCTTCCTCGCTCACTGACTGCTGCGCTCGT 14289  
QY 1476 C...TTGCGGCTGCGCGAGCGGTATCAGCTCACTCAAGCGGTAATACGGTTATCCACAGA 4535  
D2 1290 C...TTGCGGCTGCGCGAGCGGTATCAGCTCACTCAAGCGGTAATACGGTTATCCACAGA 14349  
QY 1536 A...TCAGGGATACGAGGAAAGAAATGTGAGCAAAAGCCAGCAAAAGCGCAGAACCG 4595  
D2 1350 A...TCAGGGATACGAGGAAAGAAATGTGAGCAAAAGCCAGCAAAAGCGCAGAACCG 14409  
QY 1596 T...AAAAGCGCGGTTGCTGGCGGTTTTTCCATAGGCTCCGCCCTCGAGCATCAAA 4655  
D2 1410 T...AAAAGCGCGGTTGCTGGCGGTTTTTCCATAGGCTCCGCCCTCGAGCATCAAA 14469  
QY 656 A...ATCGACGCTCAAGTCAGAGTGCGGAAACCCGACAGGACTATAAGATACCGGCGGT 4715  
D2 1470 A...ATCGACGCTCAAGTCAGAGTGCGGAAACCCGACAGGACTATAAGATACCGGCGGT 14529  
QY 1716 T...CCCTGGAAGCTCCCTGCGGCTCTCTGTTTCGACCTCGCGCTTACCGGATACCT 4775  
D2 1530 T...CCCTGGAAGCTCCCTGCGGCTCTCTGTTTCGACCTCGCGCTTACCGGATACCT 14589  
QY 1776 C...CCGCTTTTCCCTTCGGGAAGGCTGGCGCTTCTCATAGCTCACTGCTAGGTATCT 4835  
D2 1590 C...CCGCTTTTCCCTTCGGGAAGGCTGGCGCTTCTCAATGCTCACGCTGAGGTATCT 14649  
QY 836 C...GTTTCGCTGAGGTGCTTCGCTCCAAAGTGGGCTGTGTGACGAAACCCCGCTTCAGCC 4895  
D2 650 C...GTTTCGCTGAGGTGCTTCGCTCCAAAGTGGGCTGTGTGACGAAACCCCGCTTCAGCC 14709

QY 4896 CGACCGCTGCGGCTTATTCGGTAACTATCGTTCAGTCCACCCGGTAAGACA 4955  
D2 14710 CGACCGCTGCGGCTTATTCGGTAACTATCGTTCAGTCCACCCGGTAAGACA 4955 14759  
QY 4956 ATCGCCTCTGCGAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAGG 5015  
D2 14770 ATCGCCTCTGCGAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAGG 5015 14829  
QY 5016 TACAGAGTCTTGAAGTGGTGGCTTAACCTACGGCTACACTAGAAAGACAGTATT 5075  
D2 14830 TACAGAGTCTTGAAGTGGTGGCTTAACCTACGGCTACACTAGAAAGACAGTATT 5075 14889  
QY 5076 CTGCGCTCTGCTGAAGCCAGTTTACCTTCGGAAAAAGAGTTTGTAGCTCTTGTATC 5135  
D2 14890 CTGCGCTCTGCTGAAGCCAGTTTACCTTCGGAAAAAGAGTTTGTAGCTCTTGTATC 5135 14949  
QY 5136 ACAAACCAACCGCTGGTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATTACGCG 5195  
D2 14950 ACAAACCAACCGCTGGTAGCGGTGTTTTTTTGTTCGAAGCAGCAGATTACGCG 5195 15009  
QY 5196 AAAAGGATCTCAAGAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTG 5255  
D2 15010 AAAAGGATCTCAAGAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTG 5255 15069  
QY 5256 AAACCTCAGCTTAAAGGATTTTGGTCAACAGATTATCAAAAAGGATCTTCACTAT 5315  
D2 15070 AAACCTCAGCTTAAAGGATTTTGGTCAACAGATTATCAAAAAGGATCTTCACTAT 5315 15129  
QY 5316 TTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTG 5375  
D2 15130 TTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTG 5375 15189  
QY 5376 CAGTTTACCAATGCTTAATCAGTGAGGACACCTATCTCAGCGATCTGTCTATTTCG 5435  
D2 15190 CAGTTTACCAATGCTTAATCAGTGAGGACACCTATCTCAGCGATCTGTCTATTTCG 5435 15249  
QY 5436 CATAGTTGCTGACTCCCGCTGCTGTAGATAAATCAATCTAAAGTATATATGAGTAAACTTG 5495  
D2 15250 CATAGTTGCTGACTCCCGCTGCTGTAGATAAATCAATCTAAAGTATATATGAGTAAACTTG 5495 15309  
QY 5496 CCCAGTGCTGCAATGATACCGCGAGACCCAGCTACCGGCTCCAGATTATCT 5555  
D2 15310 CCCAGTGCTGCAATGATACCGCGAGACCCAGCTACCGGCTCCAGATTATCT 5555 15369  
QY 5556 AAACCAAGCAGCCGAGGCGGAGCGAGCGAGAGTGGTCTCTCAACTTTTATCCGCT 5615  
D2 15370 AAACCAAGCAGCCGAGGCGGAGCGAGCGAGAGTGGTCTCTCAACTTTTATCCGCT 5615 15429  
QY 5616 CCAGTCTATTAAATTTGTTCCCGGAGCTAGAGTAAGTAGTTTCGCCAGTTAATAG 5675  
D2 15430 CCAGTCTATTAAATTTGTTCCCGGAGCTAGAGTAAGTAGTTTCGCCAGTTAATAG 5675 15489  
QY 5676 CAAAGTTGTTGCCATTCGCTACAGGATCGTGGTGTACGCTCGCTGCTTTGGTAT 5735  
D2 15490 CAAAGTTGTTGCCATTCGCTACAGGATCGTGGTGTACGCTCGCTGCTTTGGTAT 5735 15549  
QY 5736 ATTACAGCTCCCGTTCCCAACGATCAAGCGAGTTTACATGATCCCGCATGTTGTG 5795  
D2 15550 ATTACAGCTCCCGTTCCCAACGATCAAGCGAGTTTACATGATCCCGCATGTTGTG 5795 15609  
QY 5796 AGCGGTTAGCTCTCTCGGCTCCCGCTGCTGTTGTGAGAAAGTAAAGTTGGCCGAGTC 5855  
D2 15610 AGCGGTTAGCTCTCTCGGCTCCCGCTGCTGTTGTGAGAAAGTAAAGTTGGCCGAGTC 5855 15669  
QY 5856 ACTCATGGTTATGCGAGCAGCTGCAATTTCTCTTACTGTATGCCATCCGTAAGT 5915  
D2 15670 ACTCATGGTTATGCGAGCAGCTGCAATTTCTCTTACTGTATGCCATCCGTAAGT 5915 15729  
QY 5916 TTTCTGCTGACTGGTGAGTACTCAACCAAGTCAATCTCTGAGAAATAGTGTATGCGGCG 5975  
D2 15730 TTTCTGCTGACTGGTGAGTACTCAACCAAGTCAATCTCTGAGAAATAGTGTATGCGGCG 5975 15789

POLOGY: linear

3 DESCRIPTION: SEQ ID NO: 1:

56.1%; Score 3578.4; DB 4; Length 16656;  
ilarity 88.9%; Pred. No. 0;  
Conservative 0; Mismatches 16; Indels 503; Gaps 5;

3CTCAGCTTTCTAGGCGGAAAGAACAGCTGGGGCTCTAGGGGATATCCCCAGC 1809  
3CTCTATGGCTTTCTAGGCGGAAAGAACAGCTGGGGCTCTAGGGGATATCCCCAGC 12058  
CTGTAGCGCGCATTAAGCGCGGGGTGTGTGTACGCGCAGCGTACCGGTAC 1869  
CTGTAGCGCGCATTAAGCGCGGGGTGTGTGTACGCGCAGCGTACCGGTAC 12118  
TTGCCAGCGCTTAGCGCGCTCTCTTTGCTTTCTTCCCTTCTCTTCTCGCCAGTT 1929  
TTGCCAGCGCTTAGCGCGCTCTCTTTGCTTTCTTCCCTTCTCTTCTCGCCAGTT 12178  
CGGCTTTCCCGCTCAGCTCTAAATCGGGC-TCCCTTTAGGTTCCGATTTAGTC 1988  
CGGCTTTCCCGCTCAGCTCTAAATCGGGCATCCCTTTAGGTTCCGATTTAGTC 12238  
TACGCACTCTGACCCCAAAAATCTGATTAGGGTATGGTTCACTAGTGGCCATC 2048  
TACGCACTCTGACCCCAAAAATCTGATTAGGGTATGGTTCACTAGTGGCCATC 12298  
CTGTAGAGCGTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTTAAATAGTACT 2108  
CTGTAGAGCGTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTTAAATAGTACT 12358  
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TGTTCCAACTGGAACACACTCAACCTCTCTCGTCTCTTCTTTTGAATTAAG 12418  
TTTTGCCGATTTTCGGCTATTGGTTAAAAAATGAGCTGATTTAAACAAAATTAACGC 2228  
TTTTGGGATTTTCGGCTATTGGTTAAAAAATGAGCTGATTTAAACAAAATTAACGC 12478  
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GGCGGAAGAACCACTGTGGAAATGTGTGTGCTAGTTAGGGTGTGGAAAGTCCCGGCT 2348  
-----CTGTGGAAATGTGTGTGCTAGTTAGGGTGTGGAAAGTCCCGGCT 12530  
CCA-GCAGGAGAGATATCAAAAGCATGCTCTCAATTAGTCAGCAACCAAGGTGTGGA 2407  
CCAGGAGGAGAGATATCAAAAGCATGCTCTCAATTAGTCAGCAACCAAGGTGTGGA 12590  
GTCCGAGGCTCCCGAGGAGAGATATGCAAAAGCATGCTCTCAATTAGTCAGCA 2467  
GTCCGAGGCTCCCGAGGAGAGATATGCAAAAGCATGCTCTCAATTAGTCAGCA 12650  
CATAGTCCCGCCCTAACTCCGCCATCCGCCCTAACTCCGCCAGTTCGCCCAT 2527  
CATAGTCCCGCCCTAACTCCGCCATCCGCCCTAACTCCGCCAGTTCGCCCAT 12710  
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TCGCCCATAGGCTGACTAATTTTATTTATGAGAGGCGGAGCGCCCTCGGCC 12770  
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TGAGCTATTCAGAGTAGTAGGAGGCTTTTGGAGGCTTAGGCTTTTGGAGAT 12830  
-----GATCAAGAGACAGGATGAGGATCGTTT 2675  
CCGGGAGCTTGTATATCAATTTTCGGATCTGATCAAGAGACAGGATGAGGATCGTTT 12890  
CATGATTGAACAGATGAGATGCAACAGGTTCTCGGCCGCTTGGGTGGAGAGGCTA 2735

Db 12891 CGCATGATTGAACAAGATGATTGCAACGAGTTTCTCGGCGGCTTGGGTGGAG  
QY 2736 TTGGCTATGATCGGGCAACAAGCAATCGGCTGCTCTGATCGCGCGGTGTTTC  
Db 12951 TTGGCTATGATCGGGCAACAAGCAATCGGCTGCTCTGATCGCGCGGTGTTTC  
QY 2796 TCAGCGCAGGGCGCGCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTG  
Db 13011 TCAGCGCAGGGCGCGCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTG  
QY 2856 CTGCAAGACGAGGCGCGGCTATCGTGGCTGGCCACGACGGGCTTCTTTC  
Db 13071 CTGCAAGACGAGGCGCGGCTATCGTGGCTGGCCACGACGGGCTTCTTTC  
QY 2916 GTGCTCAGCGTTGTCACTGAAGCGGGAAGGGACTGGCTGTATTTGGGGAAGTG  
Db 13131 GTGCTCAGCGTTGTCACTGAAGCGGGAAGGGACTGGCTGTATTTGGGGAAGTG  
QY 2976 CAGGATCTCTGTCTCATCTCACTTGTCTCCGCGAGAAAGTATCCATCATGGCT  
Db 13191 CAGGATCTCTGTCTCATCTCACTTGTCTCCGCGAGAAAGTATCCATCATGGCT  
QY 3036 ATGCGCGGCTGCATACGCTTGTATCCGCTACTCTGCCCATTTGCAACCAAGCG  
Db 13251 ATGCGCGGCTGCATACGCTTGTATCCGCTACTCTGCCCATTTGCAACCAAGCG  
QY 3096 CGCATCAGCGGACGCTACTCTCGATCGGAGCGGCTCTTGTGATCAGGATGAT  
Db 13311 CGCATCAGCGGACGCTACTCTCGATCGGAGCGGCTCTTGTGATCAGGATGAT  
QY 3156 GAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCGAGGCTCAAGCGGAGC  
Db 13371 GAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCGAGGCTCAAGCGGAGC  
QY 3216 GACGCGAGGATCTCGTGTGTGACCCATGGGATGCTCTGCTTGCAGAAATATCATG  
Db 13431 GACGCGAGGATCTCGTGTGTGACCCATGGGATGCTCTGCTTGCAGAAATATCATG  
QY 3276 AATGCGCGCTTTTCTGATTTTCATGACTGTGGCGGCTGGGTGGGAGCGCG  
Db 13491 AATGCGCGCTTTTCTGATTTTCATGACTGTGGCGGCTGGGTGGGAGCGCG  
QY 3336 GACATAGCTTTGGCTAGCCGCTGATTTGCTGAAGAGCTTGGCGGCAATGGGCT  
Db 13551 GACATAGCTTTGGCTAGCCGCTGATTTGCTGAAGAGCTTGGCGGCAATGGGCT  
QY 3396 TTCTCTGTGCTTTACGGTATCGCGCTCCCGATTCGCAAGCGCATCGCCTTCTAT  
Db 13611 TTCTCTGTGCTTTACGGTATCGCGCTCCCGATTCGCAAGCGCATCGCCTTCTAT  
QY 3456 CTGCAAGGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGGGA  
Db 13671 CTGCAAGGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGGGA  
QY 3516 ACCTGCGCATCAGGATTTGATTTCCACCGCGGCTTCTATGAAAGGTGGGCT  
Db 13731 ACCTGCGCATC-----  
QY 3576 TCGTTTTCCGGGAACGCGGCTGGATGATTCCTCCAGCGCGGGGATCTCATGTGG  
Db 13741 -----  
QY 3636 TCGCCCACTTAGGGGAGGCTTAATGAAACACGGAAGGAGACAATACCGGAAG  
Db 13741 -----  
QY 3696 CGCATGACGCAATAAAAAACAGAAATAAAACGCACGGTGTGTGGGTGTTTGT  
Db 13741 -----  
QY 3756 ACGCGGGGTTCCGTTCCAGGGCTGGCACTCTGTGTGATACCCCAACGAGACCGCA



Dc	1590	GTCGCGCCTTCTCCCTTCGCGAAAGCGTGGCGCTTTTCTCAATGCTCACGCTGTAGGTATCT	14649
Qy	1836	CAGTTCCGGTGTAGTTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGCTTCAGCC	4895
Dc	1851	CAGTTCCGGTGTAGTTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGCTTCAGCC	14709
Qy	1856	CACCGCTGGCCTTATCCGGTAACTATCGTCTTTGAGTCCAAACCCGGTAAAGACACGACTT	4955
Dc	1711	CACCGCTGGCCTTATCCGGTAACTATCGTCTTTGAGTCCAAACCCGGTAAAGACACGACTT	14769
Qy	1956	ATCGCCACTCGCAGCGCACTCGTAAACAGGATTACGACGAGGAGGTATGTAGGCGGTGC	5015
Dc	1776	ATCGCCACTCGCAGCGCACTCGTAAACAGGATTACGACGAGGAGGTATGTAGGCGGTGC	14829
Qy	1916	TACAGAGTCTTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTAT	5075
Dc	1830	TACAGAGTCTTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTAT	14889
Qy	1976	CTGGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGTAGCTCTTGATCCGGCAA	5135
Dc	1890	CTGGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGTAGCTCTTGATCCGGCAA	14949
Qy	1136	ACTAAACACACGCTGGTAGCGGTGGTTTTTTTGTTCAGACGACAGATTACGCGCAGAAA	5195
Dc	1950	ACTAAACACACGCTGGTAGCGGTGGTTTTTTTGTTCAGACGACAGATTACGCGCAGAAA	15009
Qy	1196	AAAGGATCTCAAGAAGATCCTTTTGATCTTTTTCTAGCGGCTCTGACGCTCAGTCGAAAGA	5255
Dc	1010	AAAGGATCTCAAGAAGATCCTTTTGATCTTTTTCTAGCGGCTCTGACGCTCAGTCGAAAGA	15069
Qy	1256	AAACTCAGTTAAGGANTTTGGTCTATGAGATTATCAAAAAAGATCTTCACTAGATCCT	5315
Dc	1070	AAACTCAGTTAAGGANTTTGGTCTATGAGATTATCAAAAAAGATCTTCACTAGATCCT	15129
Qy	316	TTTAAATTAATAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGA	5375
Dc	1230	TTTAAATTAATAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGA	15189
Qy	1376	CAGTTACCAATGCTTAATCAGTCAGGCGACCTATCTCAGCGATCTGTCTATTTCTGTTCAATC	5435
Dc	1190	CAGTTACCAATGCTTAATCAGTCAGGCGACCTATCTCAGCGATCTGTCTATTTCTGTTCAATC	15249
Qy	1436	CATAGTTGCCCTGACTCCCGCTCGTGTAGATAACTACGATACGGGAGGCTTACCATCTGG	5495
Dc	1250	CATAGTTGCCCTGACTCCCGCTCGTGTAGATAACTACGATACGGGAGGCTTACCATCTGG	15309
Qy	486	CTCCAGTGTGCAATGATACCGGAGACCCACGCTCACCGGCTCCAGATTATCAGCAAT	5555
Dc	1310	CTCCAGTGTGCAATGATACCGGAGACCCACGCTCACCGGCTCCAGATTATCAGCAAT	15369
Qy	1556	AAACACGACCGCGAAGGGCCGAGGCGAGAGTGGTCTCTGCAAATTTATCCGCTCCAT	5615
Dc	1370	AAACACGACCGCGAAGGGCCGAGGCGAGAGTGGTCTCTGCAAATTTATCCGCTCCAT	15429
Qy	1616	CCAGTCTATTAAATTTGTTCCGGGAAGCTAGATAAGTATTGCGCAGTTAATFAGTTTCGG	5675
Dc	1430	CCAGTCTATTAAATTTGTTCCGGGAAGCTAGATAAGTATTGCGCAGTTAATFAGTTTCGG	15489
Qy	1676	CAACGTTGTTGCCATTCGCTACAGGCATCGTGGTGTACAAGTCCCGCTGGTGGTATGGCTTC	5735
Dc	1490	CAACGTTGTTGCCATTCGCTACAGGCATCGTGGTGTACAAGTCCCGCTGGTGGTATGGCTTC	15549
Qy	1736	ATTACGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTGTGTGCAAAA	5795
Dc	1550	ATTACGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTGTGTGCAAAA	15609
Qy	1796	AGCGGTTAGCTCCTTCGGTCCGATCGTTGTGCAGAGTAAAGTTGGCCGACGTGTTATC	5855
Dc	1610	AGCGGTTAGCTCCTTCGGTCCGATCGTTGTGCAGAGTAAAGTTGGCCGACGTGTTATC	15669
Qy	1856	ATTATCGTTATGGCAGCATGCTAATTTCTCTTATCTGTATGCCATCCGTAAGATGCTT	5915
Dc	1670	ATTATCGTTATGGCAGCATGCTAATTTCTCTTATCTGTATGCCATCCGTAAGATGCTT	15729

## RESULT 12

US-09-350-399-1

US 03 550 333 I  
: Sequence 1. Application US/09350399

: sequence 1, Appl. No. 6342372  
: Patent No. 6342372

; FISCAL NO. 0342372  
; GENERAL INFORMATION:

APPLICANT: Dubensky Jr., Thomas W

ATTORNEY: DUBENSKY ST., 1100  
POLA. JOHN M.

Photo, COMMI M.  
Jolly. Douglas J.

Driver: David A. Douglass

DRIVER, DAVID A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEM

NUMBER OF SEQUENCES: 12

NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:

; . . . CORRESPONDENCE ADDRESS: ADDRESSER, SEED and BEPPY I.I.B.

ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center 701 Fifth Avenue

STREET: 6300 COLUMBIA  
CITY: GOATTS

; CTTY: seattle  
cmmp: week: nationSTATE: Wash  
COUNTRY: USCOUNTRY: US  
ZTD: 00104 7000; ;  
ZIP: 98104-7092  
COMMUNITY DEVELOPMENT

COMPUTER READABLE FORM:

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;
; MEDIUM TYPE: Floppy disk
;

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; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/350,399

;  
FILING DATE: 08-Jul-1999

; CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: McMASTERS, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

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TELEPHONE: (206) 682-  
TELEFAX: (206) 682-

; JEFFER: (206) 882-8  
 : INFORMATION FOR SEQ ID NO: 1:

; INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:

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; SEQUENCE CHARACTERISTICS:
      LENGTH: 16556 base pairs

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LENGTH: 16656 base p

2675	-----GATCAAGAGACAGGATGAGGATCGTTT	13741	-----
12890	CCCGGAGCTTGTAATATCCATTTTCGGATCTGATCAAGAGACAGGATGAGGATCGTTT	3756	ACGGGGGTTTCGGTCCAGGGTGGCACTCTCTGTGATACCCACACGAGACCCCA
2735	CATGATTGAAACAAGATGAGTTGCAAGCAGGTTCTCCGGCGGCTTGGGTGAGAGGCTA	13741	-----
12950	CATGATTGAAACAAGATGAGTTGCAAGCAGGTTCTCCGGCGGCTTGGGTGAGAGGCTA	3816	CCAATACGCGCGGTTTCTTCTCTTTTCCCAACCCACCCCAAGTTCCGGGTGA
2795	CGGCTATGACTGGGCACAAACAGACAAATCGGCTGCTCTGATGCGCGCGTGTTCGGGCTG	13741	-----
13010	CGGCTATGACTGGGCACAAACAGACAAATCGGCTGCTCTGATGCGCGCGTGTTCGGGCTG	3876	AGGGCTCGGACGCCAACGTCGGGGCGGAGGCCCTGTCATAGCCTCAGTGTAGTACG
2855	AGCGCAGGGGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCTGAAATGAA	13741	-----ACG
13070	AGCGCAGGGGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCTGAAATGAA	3936	CGATTCACCGCGCGCTTCTATGAAGGTTTGGGCTTCGGAAATCGTTTTCGGGA
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13130	GCAGACGAGCGAGCGCGCTATCGTGGCTGCGCCACGACGGGGGTTCTTTCGCGAGCT	3996	CTGATGATCTCTCAGCGCGGGATCTCATGTCTGAGTTCTTTCGGCCACCCCAA
2975	GCTCGACGTTGTCACTGAAGCGGGAAGGACTGGGCTGCTATTGGGCGAAAGTGCCCGGG	13810	CTGATGATCTCTCAGCGCGGGATCTCATGTCTGAGTTCTTTCGCCCAACCCCAA
13190	GCTCGACGTTGTCACTGAAGCGGGAAGGACTGGGCTGCTATTGGGCGAAAGTGCCCGGG	4056	TATTGCAAGCTTATAATGTTTCAAAATAAGCAATAGCATCAAAATTTTCACAAAA
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13250	GGATCTCTGTCACTCACTTGTCTCTGCGAGAAAGTATCCATCATCGCTGATGCA	4116	ATTTTTCATCTGCATTTCTAGTTGTGGTTTGTCCAAAATCATCAATGATATCTTA
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----- 13740  
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RESULT 10  
US-08-404-796-1  
; Sequence 1, Application US/08404796  
; Patent No. 6015686  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
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; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; APPLICANT: Belli, Barbara A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTE  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/404,796  
; APPLICATION NUMBER: 15-MAR-1995  
; FILING DATE: 435  
; CLASSIFICATION: 435  
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